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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:03:42 ; Search time 169 Seconds
(without alignments)
1096.202 Million cell updates/sec

Title: US-10-798-773-2
Perfect score: 2500
Sequence: 1 MDATIAPIRIPPEMPQYGE.....YTFEYIESGIINLPKIP 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Genesexp1990s:*
3: Genesexp2000s:*
4: Genesexp2001s:*
5: Genesexp2002s:*
6: Genesexp2003s:*
7: Genesexp2003bs:*
8: Genesexp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	479	ABB82701	Abb82701 Novel hum
2	2500	100.0	479	ADA55452	Ada55452 Human pro
3	2500	100.0	479	AAB34860	Aab34860 Human kin
4	2484	99.4	491	ADC10110	Adc10110 Human NOV
5	2248	89.9	510	ADC10108	Adc10108 Human NOV
6	1571	62.8	571	AAM38895	Aam38895 Human pol
7	1429	57.2	275	AAE16279	Aae16279 Human kin
8	1429	57.2	275	ABE65473	Abel65473 Human kin
9	1301	52.0	258	AAE07843	Aae07843 Human 278
10	1301	52.0	258	ABW00581	Abw00581 Human 278
11	1184.5	47.4	240	AAM40681	Aam40681 Human pol
12	1166	46.6	236	AAU17305	Aau17305 Novel sig
13	1166	46.6	236	ADB94013	Adb94013 Human nov
14	806	32.2	248	AAU78417	Aau78417 Human pro
15	800	32.0	226	AAU78401	Aau78401 Human pro
16	648	25.9	125	ABG59945	Abg59945 Human DIT
17	553	22.1	113	AAU17614	Aau17614 Novel sig
18	553	22.1	113	AAU17303	Aau17303 Novel sig
19	553	22.1	113	AAW85250	Aaw85250 Human imm
20	553	22.1	113	ADB94322	Adb94322 Human nov
21	553	22.1	113	ADB94011	Adb94011 Human nov
22	491	19.6	94	ABE82702	Abel82702 Novel hum
23	364.5	14.6	283	ABE83735	Abel83735 Herbicide
24	364.5	14.6	283	ADN74247	Adn74247 Thale cra
25	281	11.2	212	ABU44285	Abu44285 Protein e

RESULT 1

ABB82701
ID ABB82701 standard; protein; 479 AA.

AC ABB82701;

DT 07-MAR-2003 (first entry)

DE Novel human kinase polypeptide (NHP).

KW NHP; kinase; gene therapy; drug screening; human; enzyme.

OS Homo sapiens.

PN WO200290517-A2.

XX 14-NOV-2002.

PF 08-MAY-2002; 2002WO-US014669.

XX 09-MAY-2001; 2001US-0289727P.

XX (LEXI-) LEXICON GENETICS INC.

XX Yu X, Xie Q, Abuin A, Walke DW;

WPI; 2003-103514/09.

DR N-PSDB; ABV75301.

XX New human kinase proteins and polynucleotides, useful for cosmetic and nutraceutical applications, drug screening, clinical trial monitoring, diagnosing or treating diseases associated with biological disorders or imbalances.

XX Claim 3; Page 38-39; 40pp; English.

XX The invention relates to novel human polypeptides (NHP) having kinase activity and polynucleotides encoding them. The polynucleotides, proteins, antibodies, agonists and antagonists of the proteins are useful for drug screening, clinical trial monitoring, and diagnosing or treating diseases or disorders associated with biological disorders or imbalances. The proteins and polynucleotides are useful in cosmetic and nutraceutical applications, for identifying protein coding sequences and mapping a unique gene to a particular chromosome. The sequences of the polynucleotides and proteins can also be used as additional DNA markers for restriction fragment length polymorphism analysis, or in forensic biology. The present sequence represents a NHP kinase

ALIGNMENTS

SQ Sequence 479 AA;
Query Match 100.0%; Score 2500; DB 6; Length 479;
Best Local Similarity 100.0%; Pred. No. 5.1e-234;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATIAPIRHPPEMPQYGEENHIFELMOMLEQLLIHQEPDIPFMIQHLHRDNDNVPI 60
DB 1 MDATIAPIRHPPEMPQYGEENHIFELMOMLEQLLIHQEPDIPFMIQHLHRDNDNVPI 60
QY 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARRLYLQRTVPSALLVQ 120
DB 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARRLYLQRTVPSALLVQ 120
QY 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180
DB 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180
QY 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEHYHNRIVRVPSPKILKVI 240
DB 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEHYHNRIVRVPSPKILKVI 240
QY 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
DB 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPRDL 360
DB 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPRDL 360
QY 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
DB 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
QY 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFEYIESGIINPLPKKIP 479
DB 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFEYIESGIINPLPKKIP 479
RESULT 2
ADA55452 standard; protein; 479 AA.
XX ADA55452 standard; protein; 479 AA.
AC ADA55452;
XX 20-NOV-2003 (first entry)
DT Human protein, SEQ ID 3020.
DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX Homo sapiens.
OS Homo sapiens.
XX EP1293569-A2.
XX 19-MAR-2003.
XX 21-MAR-2002; 2002EP-00006586.
XX 14-SEP-2001; 2001JP-00328381.
XX 24-JAN-2002; 2002US-0350435P.
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX WPI: 2003-395539/38.
DR N-PSDB; ADA53813.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX Claim 14; SEQ ID NO 3020; 205pp; English.
PS The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX Sequence 479 AA;
Query Match 100.0%; Score 2500; DB 6; Length 479;
Best Local Similarity 100.0%; Pred. No. 5.1e-234;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDATIAPIRHPPEMPQYGEENHIFELMOMLEQLLIHQEPDIPFMIQHLHRDNDNVPI 60
DB 1 MDATIAPIRHPPEMPQYGEENHIFELMOMLEQLLIHQEPDIPFMIQHLHRDNDNVPI 60
QY 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARRLYLQRTVPSALLVQ 120
DB 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARRLYLQRTVPSALLVQ 120
QY 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180
DB 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180
QY 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEHYHNRIVRVPSPKILKVI 240
DB 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEHYHNRIVRVPSPKILKVI 240
QY 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
DB 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPRDL 360
DB 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPRDL 360
QY 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
DB 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
QY 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFEYIESGIINPLPKKIP 479
DB 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFEYIESGIINPLPKKIP 479
RESULT 3
AAE34860 standard; protein; 479 AA.
XX AAE34860 standard; protein; 479 AA.
AC AAE34860;
XX 28-MAY-2003 (first entry)
DT Human kinases and phosphatases (KPP)-3.
DE Human; kinase and phosphatase; KPP; enzyme; cardiovascular disorder;
KW neurological disorder; cancer; gene therapy.
XX Homo sapiens.
OS Homo sapiens.
XX Key
FH Binding-site 64..71 Location/Qualifiers
FT Binding-site /note= "ATP/GTP binding site motif A (P-loop)"
FT Binding-site 275..282 /note= "ATP/GTP binding site motif A (P-loop)"
FT Binding-site /note= "ATP/GTP binding site motif A (P-loop)"
XX

PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
 PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
 PI Ort T, Padigar M, Patturajan M, Pena CE, Rastelli L, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burgess CE, Lepley DM;
 XX WPI; 2003-210149/20.
 DR N-PSDB; ADC10109.
 XX New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions with NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.
 XX Claim 1; SEQ ID NO 130; 772dp; English.
 XX The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.
 XX Sequence 491 AA;
 SQ

Query Match 99.4%; Score 2484; DB 7; Length 491;
 Best Local Similarity 97.6%; Pred. No. 1.9e-232;
 Matches 479; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MDATIAHPHPMPQYQGEENHIFELM-----QNMLEQLLIHQEPDIPPMIQ 48
 Db 1 MDATIAHPHPMPQYQGEENHIFELMQVLTWVSALHPQNMLEQLLIHQEPDIPPMIQ 60
 Qy 49 HLHRDNDNPRVILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARLYL 108
 Db 61 HLHRDNDNPRVILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARLYL 120
 Qy 109 QRKTVPSALLVQLIOERLAEDCIKQWILDGIPETREQALRIQTLGITPRHVIVLSAPD 168
 Db 121 QRKTVPSALLVQLIOERLAEDCIKQWILDGIPETREQALRIQTLGITPRHVIVLSAPD 180
 Qy 169 TVLIERNLGRKIDPQTGEIYHTTDPPESEIQNRLMVPEDISELETAQKLLEYHRNIVR 228
 Db 181 TVLIERNLGRKIDPQTGEIYHTTDPPESEIQNRLMVPEDISELETAQKLLEYHRNIVR 240
 Qy 229 VIPSPKILKVISADQPCVDVYQALTYVQSNHRTNAPFPRVLLGLPGVSGSKSLQAALL 288
 Db 241 VIPSPKILKVISADQPCVDVYQALTYVQSNHRTNAPFPRVLLGLPGVSGSKSLQAALL 300
 Qy 289 AQKRLNVNCGQLLKQEAADRTTFGLIOPFFKEMAVPDSLLMKVLSORLDDQDCIQK 348
 Db 301 AQKRLNVNCGQLLKQEAADRTTFGLIOPFFKEMAVPDSLLMKVLSORLDDQDCIQK 360
 Qy 349 GWWLHGVRDLDOAHLNRLGYNRNVFFLNVPDSIMERLTLRIDPVTGERVHLMYKP 408
 Db 361 GWWLHGVRDLDOAHLNRLGYNRNVFFLNVPDSIMERLTLRIDPVTGERVHLMYKP 420
 Qy 409 PPTWEIQARLQNPDAEEQVKLQNDLFYRNSADLEQLYGSAILTNGDQDPYTVFYEIES 468
 Db 421 PPTWEIQARLQNPDAEEQVKLQNDLFYRNSADLEQLYGSAILTNGDQDPYTVFYEIES 480
 Qy 469 GIINPLPKKIP 479
 Db 481 GIINPLPKKIP 491

ADC10108
 ID ADC10108 standard; protein; 510 AA.
 XX AC
 AC ADC10108;
 XX AC
 DT 18-DEC-2003 (first entry)
 XX AC
 XX Human NOVX polypeptide SEQ ID NO: 128.
 XX DE
 XX KW cytotstatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.
 XX AC
 OS Homo sapiens.
 XX AC
 PN WO2003000842-A2.
 XX AC
 XX 03-JAN-2003.
 PD AC
 PF 04-JUN-2002; 2002WO-US017443.
 XX AC
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296575P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0298285P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301530P.
 PR 28-JUN-2001; 2001US-0301550P.
 PR 03-JUL-2001; 2001US-0302951P.
 PR 31-JUL-2001; 2001US-0308890P.
 PR 14-SEP-2001; 2001US-0322297P.
 PR 25-SEP-2001; 2001US-0324669P.
 PR 03-DEC-2001; 2001US-0337477P.
 PR 14-DEC-2001; 2001US-0341562P.
 PR 21-FEB-2002; 2002US-0358656P.
 PR 21-FEB-2002; 2002US-0359122P.
 PR 22-FEB-2002; 2002US-0359340P.
 PR 22-FEB-2002; 2002US-0359034P.
 PR 22-FEB-2002; 2002US-0359035P.
 PR 22-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-0359964P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 12-MAR-2002; 2002US-0363766P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.
 PR 04-JUN-2002; 2002US-00379444.
 (CURA-) CURAGEN CORP.
 XX AC
 XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
 PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
 PI Ort T, Padigar M, Patturajan M, Pena CE, Rastelli L, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burgess CE, Lepley DM;
 XX WPI; 2003-210149/20.
 DR N-PSDB; ADC10107.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX
XX Claim 1; SEQ ID NO 128; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conserving substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to one of the
CC polypeptides of the invention.
XX
XX Sequence 510 AA;

Query Match 89.9%; Score 2248; DB 7; Length 510;
Best Local Similarity 90.8%; Pred. No. 1.9e-209;
Matches 435; Conservative 0; Mismatches 0; Indels 44; Gaps 1;
QY 1 MDATIAPIPRIPPEMPQYGEENHIFELMQLLEQLLIHQPDPIPFMIQHLHRDNDNVPI 60
DB 76 MDATIAPIPRIPPEMPQYGEENHIFELMQLLEQLLIHQPDPIPFMIQHLHRDNDNVPI 135
QY 61 VILGPASGKTTIAMKLCXHLNLSLLTLENILNEFSYTATEARRLYLQKTVPSALLVQ 120
DB 136 VILGPASGKTTIAMKLCXHLNLSLLTLENILNEFSYTATEARRLYLQKTVPSALLVQ 195
QY 121 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLITPRHIVILSAPDVTLLIERNLGRKI 180
DB 196 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLITPRHIVILSAPDVTLLIERNLGRKI 255
QY 181 DPOTGEIYHTFTFWPPESIQNRLMVPDISELETAQKLLLEYHRNIVRVPSPKILKVI 240
DB 256 DPOTGEIYHTFTFWPPESIQNRLMVPDISELETAQKLLLEYHRNIVRVPSPKILKVI 315
QY 241 SADQPCVDVFPYQALTYVQSNHRTNAPTPRVLLGPGVSGKSQAALLAQKRLVNVCCG 300
DB 316 SADQPCVDVFPYQALTYVQSNHRTNAPTPRVLLGPGVSGKSQAALLAQKRLVNVCCG 375
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRDQDQCTQKGNVLHGVPRDL 360
DB 376 QL-----QKGNVLHGVPRDL 391
QY 361 QAHLLNRLGYNPNRVFFLNVPDPSIMERLTLRIDPVTGERYHMYKPPPTMEIQARLLQ 420
DB 392 QAHLLNRLGYNPNRVFFLNVPDPSIMERLTLRIDPVTGERYHMYKPPPTMEIQARLLQ 451
QY 421 NPKDAEQVKLQMDLFPYRNSADLEQYGSATLNGDDQDPTVTFEYESGINPLPKKIP 479
DB 452 NPKDAEQVKLQMDLFPYRNSADLEQYGSATLNGDDQDPTVTFEYESGINPLPKKIP 510

RESULT 6
AM38895
ID AM38895 standard; protein; 571 AA.
XX
XX AM38895;
XX
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 2040.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.
XX
XX Homo sapiens.
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00486725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSEQ-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI. 2001-442253/47.
DR N-PSDB; AAI58051.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT
XX
XX Example 3; SEQ ID NO 2040; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAI62213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 571 AA;

Query Match 62.8%; Score 1571; DB 4; Length 571;
Best Local Similarity 53.6%; Pred. No. 1.9e-143;
Matches 336; Conservative 4; Mismatches 11; Indels 276; Gaps 4;
QY 1 MDATIAPIPRIPPEMPQYGEENHIFELMQLLEQLLIHQPDPIPFMIQHLHRDNDNVPI 60
DB 1 MDATIAPIPRIPPEMPQYGEENHIFELMQLLEQLLIHQPDPIPFMIQHLHRDNDNVPI 28
QY 61 VILGPASGKTTIAMKLCXHLNLSLLTLENILNEFSYTATEARRLYLQKTVPSALLVQ 120
DB 29 -----AMKLCXHLNLSLLTLENILNEFSYTATEARRLYLQKTVPSALLVQ 75
QY 121 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLITPRHIVILSAPDVTLLIERNLGRKI 180
DB 76 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLITPRHIVILSAPDVTLLIERNLGRKI 135
QY 181 DPOTGEIYHTFTFWPPESIQNRLMVPDISELETAQKLLLEYHRNIVRVPSPKILKVI 240
DB 136 DPOTGEIYHTFTFWPPESIQNRLMVPDISELETAQKLLLEYHRNIVRVPSPKILKVI 195
QY 241 SADQPCVDVFPYQALTYVQSNHRTNAPTPRVLLGPGVSGKSQAALLAQKRLVNVCCG 300

Db 196 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKLQAALLAQKYLNVNCCG 355
QY 301 QLLKEAVADRTTGGELIQPFKEKEMA----- 326
Db 256 QLLKEAVADRTTGGELIQPFKEKEMAEGGHRVKGTVFSPRTLPCNQKDLPCLLKLEDM 315
QY 327 ----- 326
Db 316 LYLRLSELPEELLVGLPYTFGESLETSQIFLFPNPPNGRCSLKPLSLMEHPRLTGA 375
QY 327 ----- 326
Db 376 DTGSFSLGCRGHLQRCQDMRBEVAPVTLCSLYTYDQGSLLDILGPIGLQEGRDPGT 435
QY 327 -----VPDSLL 332
Db 436 QGPOEKEKQMPASPMNTDAHLDFNFKGLKERSYTGQFANVDRBERQCGCGVVDLSLL 495
QY 333 MKVLSQRLDQDCIQKGWLVHGVPRDLDOAHLNRLGYNPNRVFLLNVPFDSIMERLTUR 392
Db 496 MKVLSQRLDQDCIQKGWLVHGVPRDLDOAHLNRLGYNPNRA----- 538
QY 393 RIDPVTGERVHLMKPPPTMEIQARLL 419
Db 539 ---QLKGSRLH---KPSRVPEVECLLV 559

RESULT 7
AAE16279 ID AAE16279 standard; protein; 275 AA.
XX AC AAE16279;
XX DT 26-MAR-2002 (first entry)
XX DE Human kinase PKIN-25 protein.
XX KW Human; kinase; PKIN-25; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW fatty liver; Niemann-Pick's disease; gene therapy.
XX OS Homo sapiens.
XX KW WO200196547-A2.
XX PN 20-DEC-2001.
XX PD 14-JUN-2001; 2001WO-US019444.
XX PF 15-JUN-2000; 2000US-0212073P.
XX PR 23-JUN-2000; 2000US-0213467P.
XX PR 30-JUN-2000; 2000US-0215651P.
XX PR 07-JUN-2000; 2000US-0216605P.
XX PR 13-JUL-2000; 2000US-0218372P.
XX PR 25-AUG-2000; 2000US-0228056P.
XX PA (INCY-) INCYTE GENOMICS INC.

XX DR WPI; 2002-090207/12.
DR N-PSDB; AAD26472.
PT New polypeptides, useful for diagnosing, treating or preventing disorders
PT of growth and development, cardiovascular and lipid, and diseases such as
PT cancer, comprise human kinase polypeptides.
XX PS Claim 1; Page 173-174; 197pp; English.
XX CC The invention relates to human kinase PKIN proteins and their
CC corresponding cDNAs. A composition containing PKIN agonist is useful for
CC treating a disease or condition associated with decreased expression of
CC PKIN and a composition comprising PKIN antagonist is useful for treating
CC a disease or condition associated with overexpression of PKIN. The
CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC of a test compound and in gene therapy. The present sequence is human
CC PKIN-25 protein
XX SQ Sequence 275 AA;

Query Match 57.2%; Score 1429; DB 5; Length 275;
Best Local Similarity 100.0%; Pred. No. 4.2e-130;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 MVEDTSELETAQKLEHNRNVRVPSYKILKVISADQPCVDVYQALTYVQSNHRTN 264
Db 1 MVEDTSELETAQKLEHNRNVRVPSYKILKVISADQPCVDVYQALTYVQSNHRTN 60
QY 265 APPTPRVLLGPGVSGSKLQAALLAQKYLNVNCCQQLKEAVADRTTGGELIQPFKEK 324
Db 61 APPTPRVLLGPGVSGSKLQAALLAQKYLNVNCCQQLKEAVADRTTGGELIQPFKEK 120
QY 325 MAVPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLDOAHLNRLGYNPNRVFLLNVPFDS 384
Db 121 MAVPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLDOAHLNRLGYNPNRVFLLNVPFDS 180
QY 385 IMERLTLRRIDPVTGERVHLMKPPPTMEIQARLLNQNPKDAEPOVKLKMDFYNSADLE 444
Db 181 IMERLTLRRIDPVTGERVHLMKPPPTMEIQARLLNQNPKDAEPOVKLKMDFYNSADLE 240
QY 445 QLYGSAITLNGDQDPTVTFEYIESGIINPLPKKIP 479
Db 241 QLYGSAITLNGDQDPTVTFEYIESGIINPLPKKIP 275

RESULT 8
ADB65473 ID ADB65473 standard; protein; 275 AA.
XX AC ADB65473;
XX DT 04-DEC-2003 (first entry)
XX DE Human protein encoded by clone TESTI20244460.
XX KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;

CC diseases involving haematopoietic stem cells (e.g., leukaemia), disorders
CC involving B-cells (e.g., lymphoblastic leukaemia/lymphoma) and disorders
CC involving precursor T-cell neoplasms. 27802 sequence is useful for
CC modulating cellular growth and/or cellular metabolic pathways.
CC particularly for regulating one or more proteins involved in growth and
CC metabolism. 27802 DNA is used in gene therapy. 27802 sequence or its
CC antibody are useful in screening assays, detection assays (e.g.,
CC chromosomal mapping, tissue typing, forensic biology), preventive
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomics) and in methods of treatment
XX
SQ Sequence 258 AA;

Query Match 52.0%; Score 1301; DB 4; Length 258;
Best Local Similarity 99.6%; Pred. No. 1.le-117;
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 73 IAWLCKHLSLLTLENLILNBSYATARRLYLQKTVPSALLVQLIOERLAEEDCI 132
Db 1 MAWLCCKHLSLLTLENLILNBSYATARRLYLQKTVPSALLVQLIOERLAEEDCI 60
Qy 133 KQWILGIPETREQALRIOTLGTTPRHVIVLSAPDVLIERNLGKRIDPQTGEIYHTTF 192
Db 61 KQWILGIPETREQALRIOTLGTTPRHVIVLSAPDVLIERNLGKRIDPQTGEIYHTTF 120
Qy 193 DWPESEIQNRLMVPEDISELTAQKLLVYHRNIVRVPYKILKVISADQPCVDVFFQ 252
Db 121 DWPESEIQNRLMVPEDISELTAQKLLVYHRNIVRVPYKILKVISADQPCVDVFFQ 180
Qy 253 ALTVQSNHRTNAPFTRVLLGPGVGSKISQALLAQAQYRLVNVCCGQLLKEAVADRTT 312
Db 181 ALTVQSNHRTNAPFTRVLLGPGVGSKISQALLAQAQYRLVNVCCGQLLKEAVADRTT 240
Qy 313 FGELIQPFPEKEMA 326
Db 241 FGELIQPFPEKEMA 254

RESULT 10
ABW00581
ID ABW00581 standard; protein; 258 AA.

AC ABW00581;

DT 15-JAN-2004 (first entry)

XX Human 27802, adenylate kinase protein.

XX Human; ATPase-like protein; phosphatidylserine synthase-like protein;
KW DNA fragmentation factor-like protein; vesicle-mediated transport;
KW phospholipid scramblase-like protein; adenylate kinase protein;
KW organelle biogenesis; cell-cycle regulation; primary brain lymphoma;
KW protein degradation; splenomegaly; pulmonary embolism; Hodgkin disease;
KW atresia; tuberculosis; astrocyte; apoptosis; neurodegenerative disease;
KW DNA fragmentation; autoimmune disorder; cancer; blood clotting system;
KW immune system; haematopoietic; hypertension; systemic sclerosis;
KW atresclerosis; leukaemia; oligodendrocyte; enzyme.

XX Homo sapiens.

XX Location/Qualifiers

PH Key 13
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 27. .30
FT Domain /note= "Casein kinase II (CK2) phosphorylation site"
FT /note= "Domain 1"
FT Modified-site 41. .120
FT /note= "Domain 1"
FT Modified-site 68. .73
FT /note= "N-myristoylation site"
FT Modified-site 85. .87
FT /note= "Protein kinase C (PKC) phosphorylation site"
FT Modified-site 93. .96
FT /note= "Casein kinase II (CK2) phosphorylation site"

FT Modified-site 104. .107
FT /note= "Amidation site"
FT Modified-site 118. .121
FT /note= "Casein kinase II (CK2) phosphorylation site"
FT Modified-site 139. .142
FT /note= "Casein kinase II (CK2) phosphorylation site"
FT Modified-site 196. .198
FT /note= "Protein kinase C (PKC) phosphorylation site"
FT Domain 201. .251
FT /note= "Domain 1"
FT Binding-site 203. .210
FT /note= "ATP/GTP binding site motif"
FT Modified-site 206. .211
FT /note= "N-myristoylation site"
FT Modified-site 207. .209
FT /note= "Protein kinase C (PKC) phosphorylation site"
FT Modified-site 240. .243
FT /note= "Casein kinase II (CK2) phosphorylation site"

US2003092116-A1.

PD 15-MAY-2003.

XX 07-JUN-2002; 2002US-00165800.

XX 10-FEB-2000; 2000US-0181705P.

PR 29-FEB-2000; 2000US-0185609P.

PR 29-FEB-2000; 2000US-0185946P.

PR 29-FEB-2000; 2000US-0185947P.

PR 29-FEB-2000; 2000US-0186234P.

PR 12-FEB-2001; 2001US-00781677.

PR 21-FEB-2001; 2001US-00790179.

PR 21-FEB-2001; 2001US-00790180.

PR 22-FEB-2001; 2001US-00790838.

PR 26-FEB-2001; 2001US-00795038.

(MILL-) MILLENNIUM PHARM INC.

XX Chun M, Glucksmann MA, Kapeller-Libermann R, Meyers RE;

XX WPI; 2003-765479/72.

XX N-PSDB; AAD61170.

PT New isolated polypeptides including phosphatidylserine synthase-like
PT polypeptide useful for identifying a compound which binds and modulates
PT activity of the polypeptide useful for treating diseases, e.g. cancer.

XX Claim 8; Fig 28; Opp; English.

XX The present invention relates to novel proteins including ATPase-like
XX proteins, phosphatidylserine synthase-like proteins, DNA fragmentation
XX factor-like proteins, phospholipid scramblase-like proteins or adenylate
XX kinase proteins and polynucleotides encoding such proteins. The human
XX ATPase-like molecules are useful for modulating ATPase function. They are
XX useful in modulating organelle biogenesis, cell-cycle regulation, protein
XX degradation and vesicle-mediated transport. They are also useful for
XX treating disorders associated with aberrant ATPase-like expression or
XX activity such as splenomegaly, pulmonary embolism, atresia and primary
XX brain lymphoma. The human phosphatidylserine synthase-like molecules are
XX useful for modulating the biosynthetic pathway involving the synthesis of
XX the membrane phosphatidylserine (PS). They human phosphatidylserine
XX synthase-like molecules are useful for treating disorders associated with
XX aberrant human phosphatidylserine synthase activity such as tuberculosis,
XX astrocytes and Hodgkin disease. The human 5698, DNA fragmentation factor-
XX like molecules are useful for modulating apoptotic events, including DNA
XX fragmentation. The human 5698 molecules are useful for treating diseases
XX such as autoimmune disorders, neurodegenerative diseases and cancer. The
XX human 32621, phospholipid scramblase-like molecules are useful for
XX modulating immune, haematopoietic and blood clotting systems. They are
XX useful for treating a disorder associated with aberrant human
XX phospholipid scramblase-like protein activity such as leukaemia and
XX systemic sclerosis. The human 27802 adenylate kinase are useful for
XX modulating cellular growth and/or cellular metabolic pathways. They are

XX	02-AUG-2001.	PR	29-SEP-2000;	2000US-0236367P.
PD		PR	29-SEP-2000;	2000US-0236368P.
XX	17-JAN-2001;	PR	29-SEP-2000;	2000US-0236369P.
XX	2001WO-US001312.	PR	29-SEP-2000;	2000US-0236370P.
XX		PR	02-OCT-2000;	2000US-0236802P.
PR	31-JAN-2000;	PR	02-OCT-2000;	2000US-0237037P.
PR	04-FEB-2000;	PR	02-OCT-2000;	2000US-0237038P.
PR	24-FEB-2000;	PR	02-OCT-2000;	2000US-0237039P.
PR	02-MAR-2000;	PR	02-OCT-2000;	2000US-0237040P.
PR	16-MAR-2000;	PR	13-OCT-2000;	2000US-0239935P.
PR	17-MAR-2000;	PR	13-OCT-2000;	2000US-0239937P.
PR	18-APR-2000;	PR	20-OCT-2000;	2000US-0240960P.
PR	19-MAY-2000;	PR	20-OCT-2000;	2000US-0241221P.
PR	07-JUN-2000;	PR	20-OCT-2000;	2000US-0241785P.
PR	28-JUN-2000;	PR	20-OCT-2000;	2000US-0241786P.
PR	30-JUN-2000;	PR	20-OCT-2000;	2000US-0241787P.
PR	07-JUL-2000;	PR	20-OCT-2000;	2000US-0241808P.
PR	07-JUL-2000;	PR	20-OCT-2000;	2000US-0241809P.
PR	11-JUL-2000;	PR	20-OCT-2000;	2000US-0241826P.
PR	11-JUL-2000;	PR	01-NOV-2000;	2000US-0244617P.
PR	14-JUL-2000;	PR	08-NOV-2000;	2000US-0246474P.
PR	26-JUL-2000;	PR	08-NOV-2000;	2000US-0246475P.
PR	26-JUL-2000;	PR	08-NOV-2000;	2000US-0246476P.
PR	26-JUL-2000;	PR	08-NOV-2000;	2000US-0246477P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246478P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246523P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246524P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246525P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246526P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246527P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246528P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246532P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246609P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246610P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246611P.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246613P.
PR	14-AUG-2000;	PR	17-NOV-2000;	2000US-0249207P.
PR	18-AUG-2000;	PR	17-NOV-2000;	2000US-0249208P.
PR	22-AUG-2000;	PR	17-NOV-2000;	2000US-0249209P.
PR	22-AUG-2000;	PR	17-NOV-2000;	2000US-0249210P.
PR	22-AUG-2000;	PR	17-NOV-2000;	2000US-0249211P.
PR	23-AUG-2000;	PR	17-NOV-2000;	2000US-0249212P.
PR	30-AUG-2000;	PR	17-NOV-2000;	2000US-0249213P.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249214P.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249215P.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249216P.
PR	05-SEP-2000;	PR	17-NOV-2000;	2000US-0249217P.
PR	05-SEP-2000;	PR	17-NOV-2000;	2000US-0249218P.
PR	06-SEP-2000;	PR	17-NOV-2000;	2000US-0249244P.
PR	06-SEP-2000;	PR	17-NOV-2000;	2000US-0249245P.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249264P.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249265P.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249297P.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249299P.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249300P.
PR	08-SEP-2000;	PR	01-DEC-2000;	2000US-0250160P.
PR	08-SEP-2000;	PR	01-DEC-2000;	2000US-0250391P.
PR	12-SEP-2000;	PR	05-DEC-2000;	2000US-0251030P.
PR	14-SEP-2000;	PR	05-DEC-2000;	2000US-0251988P.
PR	14-SEP-2000;	PR	06-DEC-2000;	2000US-0256719P.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251479P.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251856P.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251868P.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251869P.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251989P.
PR	21-SEP-2000;	PR	08-DEC-2000;	2000US-0251990P.
PR	21-SEP-2000;	PR	11-DEC-2000;	2000US-0254097P.
PR	25-SEP-2000;	PR	05-JAN-2001;	2001US-0259678P.
PR	25-SEP-2000;	XX	(HUMA-) HUMAN GENOME SCI INC.	
PR	26-SEP-2000;	PA	Rosen CA, Barash SC, Ruben SM;	
PR	27-SEP-2000;	XX		
PR	27-SEP-2000;	PI		
PR	29-SEP-2000;	XX		

DR WPI: 2001-465460/50.
 DR N-PSDB; AAS27222.
 XX Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders.
 XX
 PS Claim 1; SEQ ID NO 870; 880bp; English.
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative disorders
 CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
 CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
 CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
 CC respiratory disorders, dermatological disorders, gastrointestinal disorders
 CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
 CC disease), reproductive system disorders, liver disorders (cirrhosis), as stimulators of
 CC (inflammatory disorders), liver disorders, activators of T-cells, to induce
 CC B-cell responsiveness to pathogens, activators of T-cells, to induce
 CC higher affinity antibodies, and as a means to induce tumour proliferation
 CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
 CC AAU17683 represent novel signal transduction pathway protein, amino acid
 CC sequences of the invention
 XX

Query Match 46.6%; Score 1166; DB 4; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.4e-104;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 QALRIQTLGITPRHVLVSAPDTVLIERNLGKIDPQTGRIYHTTDFWPESEIONRLMV 206
 DB 1 QALRIQTLGITPRHVLVSAPDTVLIERNLGKIDPQTGRIYHTTDFWPESEIONRLMV 60
 QY 207 PEDISELETAQKLEVHRNIVRIVPSYKILKVISADPCVDVYQALTYVQSNRTNAP 266
 DB 61 PEDISELETAQKLEVHRNIVRIVPSYKILKVISADPCVDVYQALTYVQSNRTNAP 120
 QY 267 FTRVLLGLGVSGKSLQALLAQKRYLVNVCQQLLKEAVADRTTFFGELIQPFPEKMA 326
 DB 121 FTRVLLGLGVSGKSLQALLAQKRYLVNVCQQLLKEAVADRTTFFGELIQPFPEKMA 180
 QY 327 VPDSLLMKVLSQRLDQDCIQKGVWLGHPVPRDLQAHLLNRLGYN 371
 DB 181 VPDSLLMKVLSQRLDQDCIQKGVWLGHPVPRDLQAHLLNRLGYN 225

RESULT 13
 ADB94013
 ID ADB94013 standard; protein; 236 AA.
 AC ADB94013;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human novel protein #247.
 XX
 KW human; autoimmune disease; Parkinson's disease; silicosis;
 KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
 KW immunosuppressive agent; adjuvant; enhance immune response;
 KW higher affinity antibody induction;
 KW increased serum immunoglobulin concentration.
 XX
 OS Homo sapiens.
 XX
 XX US2002169711-A1.

XX
 PD 14-NOV-2002.
 XX
 XX 17-JAN-2001; 2001US-00764868.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216847P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 22-AUG-2000; 2000US-0225758P.
 PR 30-AUG-2000; 2000US-0226868P.
 PR 01-SEP-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234597P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 01-NOV-2000; 2000US-0241809P.
 PR 17-NOV-2000; 2000US-0244617P.
 PR 08-DEC-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251858P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-719985/68.
 DR N-PSDB; ADB93390.
 XX
 PT New isolated polypeptide useful for diagnosing and treating
 PT immunosuppressive conditions such as autoimmune disease and Parkinson's
 PT disease.
 XX
 PS Claim 11; SEQ ID NO 870; 345pp; English.
 XX
 CC The invention relates to an isolated polypeptide. The polypeptide is
 CC useful for diagnosing a pathological condition or a susceptibility to a

PN WO200157190-A2.
XX
PD
XX 09-AUG-2001.
XX
PP 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QN, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman I, Goodrich R;
XX WPI; 2001-476283/51.
DR N-PSDB; AAK52534.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 237; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78123-AAW80302) that exhibit activity elating to
CC cytokine cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 226 AA;

Query Match 32.0%; Score 800; DB 4; Length 226;
Best Local Similarity 99.3%; Pred. No. 5.5e-69;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 327 VPSLLMKVLSQLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPFDSIM 386
DB 74 VPSLLMKVLSQLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPFDSIM 133

QY 387 ERLTLRRIDPVTGERVHLMYKPPPTWEIQARLLQNPDAEEQVKLKMDFYRNSADLEQL 446
DB 134 ERLTLRRIDPVTGERVHLMYKPPPTWEIQARLLQNPDAEEQVKLKMDFYRNSADLEQL 193

QY 447 YGSAITLNGQDPVTVFVEIESGIINPLPKIP 479
DB 194 YGSAITLNGQDPVTVFVEIESGIINPLPKIP 226

Search completed: March 18, 2005, 15:17:38
Job time : 173 secs

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Query Match	10.9%;	Score	273;	DB 2;	Length	212;			
Best Local Similarity	31.6%;	Pred	No. 1.2e-11;						
Matches	67;	Conservative	46;	Mismatches	85;	Indels	14;	Gaps	4;

QY	271	VLLGLPGVSGKSLQAALLAQAQYRLVNVCGQLLKAEVADRRTTGGELIQPFPEKEMAVPDS	330	
DB	3	LLINGLPGAGKGTAQAKIVEQGHVAHISTGDMFRAAMANQTEMGLAKSYIDKGEIYPDE	62	
QY	331	LLMKVLSQRLDQDCTQKGVNLHGVPDRDLDOAHILNR---	LGYNPNRVFFLNVPPDSIM	386
DB	63	VTNGIVKVERLSQDDIKETGFLPDGVPRTTEQAHADKTKLAEGLTEGCVINIEVNPDSLL	122	
QY	387	ERLLRLRIDPVTGERVHLMKPPPTMEIQARLLQNPKDAEQQVKLQMDLFYRNSADLEQL	446	
DB	123	ERLSGRILHRTVGETFHKVFNPPVDYK-BEDYYQREDDKPEVTKRDLV--	NIAQGEPI	178
QY	447	Y-----GSAITLNGQDDPYTFEYIESGIIN	472	
DB	179	IAHYRANGLVHDIEGNDINDVFSIEKVLTN	210	

RESULT 4	
B97898	adenylate kinase (BC 2.7.4.3) [imported] - Streptococcus pneumoniae (strain R6)
C:Species:	Streptococcus pneumoniae
C:Date:	22-Oct-2001
C:Accession:	B97898
C:Authors:	Roskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoffff
C:Title:	Genome of the Bacterium Streptococcus pneumoniae Strain R6.
C:Reference number:	A97872; MUID:21429245; PMID:11544234
C:Accession:	B97898
C:Status:	preliminary
C:Molecule type:	DNA
C:Residues:	1-212 <KUR>
C:Cross-references:	UNIPROT:Q8DRD4; GB:AE007317; PIDN:AAK99014.1; PID:g15457755
C:Genetics:	
C:Gene:	adk
C:Superfamily:	adenylate kinase
C:Keywords:	phosphotransferase

Query Match	10.9%;	Score	272;	DB 2;	Length	212;			
Best Local Similarity	31.1%;	Pred	No. 1.4e-11;						
Matches	67;	Conservative	47;	Mismatches	85;	Indels	14;	Gaps	4;

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331 LMKVLSORLDQDCIQKGVWLVHGVPPDLQAOHLNR---LGVNPNRVFFLNVPFDSIM 386
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 VTNGIVTKERLSQDDIKETGFLDDGYPTTICQAHALDKTLAELGIELEGINIEVNPDSL 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
387 ERLTLRLRIDPVTGERYHLMYKPPPTMTSIOARLLONPKDAEEQVKLWMDLFPYRSADLEQL 446
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
123 ERLSGRIIHRVTGETFHKVPFVDYK-EEDYYQREDDKPTVKRRLDV---NIAQGEPI 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
447 Y-----GSAITLNGDQDPVTYVFEVIESGIIN 472
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 IAHYRAKGLVHDIEGNQDINDVFSDDIEKVLTN 210
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
T44404
adenylate kinase (EC 2.7.4.3) [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44404; C83669
R:Takami, H.; Takaki, Y.; Nakasone, K.; Hirano, C.; Inoue, A.; Horikoshi, K.
Biochem Biotechnol. Biochem. 63, 452-455, 1999

```

A>Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A/Reference number: 222756; MUID:99209008; PMID:10192928
A/Accession: Y44404
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-217 <TAK>
A/Cross-references: UNIPROT:P38372; EMBL:AB017508; NID:94512395; PIDN:BA075292.1; PID:94
A/Experimental source: strain C-125
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: C83669
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-217 <STO>
A/Cross-references: GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA03874.1; GSPDB:GN00
A/Experimental source: strain C-125
C/Genetics:
A/Genes: adk
C/Superfamily: adenylate kinase
C/Keywords: phosphotransferase

Query Match 10.9%; Score 272; DB 2; Length 217;
Best Local Similarity 31.3%; Pred. No. 1.4e-11;
Matches 66; Conservative 42; Mismatches 83; Indels 20; Gaps 5;

QY 271 VLLIGPVSGSKLQALLAOKYRLVNVCGQLLKAVADRTTFGELIQPFKEKMAVPDS 330
DB 3 LILMLPGAGKGTQAEIKIIEYGIPIHSTGDMFRAAMKNETELGLKAKSYMDAGELVPDE 62

QY 331 LLMKVLRSQDDQCIQKGVHLGVPRDLQAHLL-----NRLGYNPNRVFFLNVPF 382
DB 63 VTIGVRLDSQDDC-QNGFLDGFPRTPVAQAEALDILASLDKLDY---VINIDVPE 117

QY 383 DSIMERLTRIDPVTGERHYLMYKPPPTMEI-----QARLLQNPKDAEQVKLMDLFR 438
DB 118 QLLMDRLTGRVSPSTGRTHVFNPPKVEGICVDGSELIQRDDDKPFTVKRLEVNQK 177

QY 439 NSADLEQLY---GSAITLNGDDPVTVEYI 466
DB 178 QAQLPDLFSEKGYLQNINGDDQISRKFEDI 208

RESULT 6
H97282
adenylate kinase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: H97282
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: H97282
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-215 <KUR>
A/Cross-references: UNIPROT:Q97EU9; GB:AE001437; PIDN:AAK81051.1; PID:G15026178; GSPDB:G
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Genes: CAC3112
C/Superfamily: adenylate kinase

Query Match 10.4%; Score 260; DB 2; Length 215;
Best Local Similarity 27.6%; Pred. No. 9.5e-11;
Matches 60; Conservative 52; Mismatches 79; Indels 26; Gaps 5;

QY 270 RVLLIGPVSGSKLQALLAOKYRLVNVCGQLLKAVADRTTFGELIQPFKEKMAVPD 329
DB 2 KIILLGPGAGKGTQAKLISSEFSIPHISTGDIIFRANISGKTELGMKAKGYMDKGLLVPD 61

A>Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A/Reference number: 222756; MUID:99209008; PMID:10192928
A/Accession: Y44404
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-217 <TAK>
A/Cross-references: UNIPROT:P38372; EMBL:AB017508; NID:94512395; PIDN:BA075292.1; PID:94
A/Experimental source: strain C-125
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: C83669
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-217 <STO>
A/Cross-references: GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA03874.1; GSPDB:GN00
A/Experimental source: strain C-125
C/Genetics:
A/Genes: adk
C/Superfamily: adenylate kinase
C/Keywords: phosphotransferase

Query Match 10.3%; Score 257.5; DB 2; Length 214;
Best Local Similarity 29.6%; Pred. No. 1.4e-10;
Matches 55; Conservative 47; Mismatches 73; Indels 11; Gaps 3;

QY 270 RVLLIGPVSGSKLQALLAOKYRLVNVCGQLLKAVADRTTFGELIQPFKEKMAVPD 329
DB 2 RIILLGAGAGKGTQAEIKIIEYGIPIHSTGDMFRAAMKNETELGLKAKSYMDAGELVPDE 61

QY 330 LLMKVLRSQDDQCIQKGVHLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
DB 62 DIILLGKIKERIAQADC-EKGLDGFPRTPQADGLKENGINVDYVIEFDVADDVIVERM 120

QY 390 TLRIDPVTGERHYLMYKPPPTMEIQAR-----LLQNPKDAEQVKLMDLFRNSAD 442
DB 121 AGRRALPSPGRTYHVVNPP---KVEGKDDVTGDELIVREDDKSTVRLVRLVHTQTAP 177

QY 443 LEQLYG 448
DB 178 LIEYTG 183

RESULT 8
S43016
adenylate kinase (EC 2.7.4.3) - Bordetella pertussis
N/Alternate names: ATP-AMP transphosphorylase
C/Species: Bordetella pertussis
C/Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S43016
R/Gilles, A.M.; Sismeiro, O.; Munier, H.; Fabian, H.; Mantsch, H.H.; Surewicz, W.K.; Cra
Eur. J. Biochem. 218, 921-927, 1993
A/Title: Structural and physico-chemical characteristics of Bordetella pertussis adenyly
A/Reference number: S43016; MUID:94109391; PMID:8281944
A/Accession: S43016
A/Molecule type: DNA
A/Residues: 1-218 <GIL>
A/Cross-references: UNIPROT:P39068; EMBL:Z29715; NID:9453620; PIDN:CAA82801.1; PID:G4536
A/Experimental source: strain 18323

C;Genetics:
A;Gene: ask
C;Function:
A;Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A;Note: magnesium required
C;Superfamily: adenylate kinase
C;Keywords: ATP; p-loop; phosphotransferase
F;7-14/Region: nucleotide-binding motif A (p-loop) #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
F;30-84/Region: Active site: Ser, Asp, His #status predicted

Query Match 10.3%; Score 256.5; DB 2; Length 218;
Best Local Similarity 32.1%; Pred. No. 1.7e-10;
Matches 59; Conservative 34; Mismatches 86; Indels 5; Gaps 2;

QY 270 RVLLGPGVSGKSLQALLAQKVRLNVNCCGLLKEAVADRTTFGBLIOPFFEKEMAVPD 329
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 2 RLILLGPPGAGKGTOAAFLTHQHGIPOISTGDMLRAAVKAGTPIGLEAKKVM DAGLVSD 61

QY 330 SLIMKVLRSQLDDQCITQGVNLHGVRPRDLDQAHLNLRGYNNRVFFLNVPFDSIMERL 389
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 DLIIGLVDRLTQPDC -ANGYLFGDPERTIPQADALKSAGIALDYVVEIEVPESDIIRM 120

QY 390 TLRIDPVTERHYLMKKPTTWIQQ-----ARLLNPDAEEOVKLKMDDL FYRNSADLEQ 445
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 SERVHPASGRSYHREPNFPKAEGVDVTGEPLVQRDDDEETVRHLNVYQNTRPLVD 180

QY 446 LYGS 449
 |||
Db 181 YYS 184

RESULT 9
G70307
adenylate kinase (EC 2.7.4.3) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70307
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; PMID:98196666; PMID:9537320
A;Accession: G70307
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-206 <AQ>
A;Cross-references: UNIPROT:O66490; GB:AEO00672; NID:g2982810; PIDN:AAC06438.1; PID:g2982810
A;Experimental source: strain VF5
C;Genetics:
A;Gene: kad
C;Function:
A;Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A;Note: magnesium required
C;Superfamily: adenylate kinase
C;Keywords: ATP; p-loop; phosphotransferase
F;7-14/Region: nucleotide-binding motif A (p-loop) #status atypical
F;77-82/Region: nucleotide-binding motif B #status atypical
F;28,81/Active site: His, Asp #status predicted

Query Match 10.2%; Score 255.5; DB 2; Length 206;
Best Local Similarity 30.9%; Pred. No. 1.8e-10;
Matches 56; Conservative 42; Mismatches 72; Indels 11; Gaps 3;

QY 271 VLLGPGVSGKSLQALLAQKVRLNVNCCGLLKEAVADRTTFGBLIOPFFEKEMAVPDS 330
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 3 LVFLGPPGAGKGTOAKRLAKEGVHISITGDLIREAVQKGTPLGKAKKEYMERGELVDPD 62

QY 331 LLMKVLRSQLDDQCITQGVNLHGVRPRDLDQA-----HLNLRGYNNRVFFLNVPFDSIM 386
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 63 LIATLEEVPFKGNV----IFDGFRFTVKQAEALDMLEKKLGKLVHDHVLLPEVDFEVI 118

QY 387 ERUTLRRIDPVTERHYLMKKPTTWIQQALLNQNKPAEEQVCLKWMDLFYRNSADLEQ 446

Db 119 ERLSGRRINPETGEVHVKNPPIPPPP---GVKVIORDDKPEVKKRLEVYEQAPLLEY 175

QY 447 Y 447

Db 176 Y 176

RESULT 10

JS0492

adenylate kinase (EC 2.7.4.3) - Bacillus subtilis

N;Alternate names: ATP-AMP transphosphorylase

C;Species: Bacillus subtilis

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS0492; S12684; S08630; E69583

A; Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yamane, K.

J. Biochem. 107, 603-607, 1990

A;Title: Cloning and characterization of a Bacillus subtilis gene homologous to E. coli

A;Reference number: JS0490; MUID: 90292990; PMID: 2113521

A;Accession: JS0492

A;Molecule type: DNA

A;Residues: 1-217 <NAK>

A;Cross-references: UNIPROT:P16304; GB:D00619; NID:G216336; PIDN:BAA00496.1; PID:G216340

R;Yoshikawa, H.; Doi, R.H.

Nucleic Acids Res. 19, 1647, 1990

A;Title: Sequence of the Bacillus subtilis spectinomycin resistance gene region.

A;Reference number: S12680; MUID: 90221911; PMID: 2139212

A;Accession: S12684

A;Molecule type: DNA

A;Residues: 1-116 <YOS>

A;Cross-references: EMBL:M31102; NID:G1184272; PIDN:AAB59119.1; PID:G143579

A;Experimental source: strain 14241

R;Sub, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.

Mol. Microbiol. 4, 305-314, 1990

A;Title: Isolation of a secY homologue from Bacillus subtilis: evidence for a common pro

A;Reference number: S08628; MUID: 90251170; PMID: 2110998

A;Accession: S08630

A;Molecule type: DNA

A;Residues: 1-99 <SUH>

A;Cross-references: EMBL:X51329; NID:G40132; PIDN:CAA357113.1; PID:G40135

A;Experimental source: strain Marburg; cell line PB2

R;Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

A;Authors: Foulger, D.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; I

ech, J.; Harwood, C.R.; Henaut, A.; Krogsh, S.; Kumano, M.; Kurita, K.; Lardinois,

Koetter, P.; Konningstein, G.; Lazarevic, V.; Lee, S.H.; Levine, A.; Liu, H.; Masuda, S.; Maue

A;Authors: Lauber, J.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Y, M.; Ogawa, K.; Ogihara, C.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

Rieger, M.; Rivolta, S.; Schroeter, R.; Scoffone, F.; Segiguchi, J.; Sekowska, A.; Sror

A;Authors: Schleich, S.; Schroeter, R.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

akeuchi, M.; Tamakoshi, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

T.; Winters, P.; Wipat, A.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Authors: Yoshikawa, H.F.; Zumstein, E.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID: 98044033; PMID: 9384377

A;Accession: E69583

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-217 <KUN>

A;Cross-references: GB:Z99104; GB:AL009126; NID:G2632267; PIDN:CAB11913.1; PID:G2632404

A;Experimental source: strain 168

C;Genetics:

A;Gene: adk

C;Function:

A;Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A;Note: magnesium required

C;Superfamily: adenylate kinase

C;Keywords: ATP; P-loop; phosphotransferase

F;7-14/Region: nucleotide-binding motif A (p-loop) #status atypical

F;80-85/Region: nucleotide-binding motif B #status atypical

F;28 84/Active site: His. Asp #status predicted

Query Match 10.0%; Score 249; DB 2; Length 217;
Best Local Similarity 30.4%; Pred. No. 5.5e-10;
Matches 62; Conservative 41; Mismatches 89; Indels 12; Gaps 4;
QY 271 VLLGPGVSGKSLQAALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPDS 330
D 271 VLLGPGVSGKSLQAALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPDS 330
Db 3 LVLMGLPGAGKGTQSEIVEDYGHISTGDMFRAMKEETPLGLEAKSYIDGELVPDE 62
QY 331 LLMKVLSORLDQDCIQKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIM 386
D 331 LLMKVLSORLDQDCIQKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIM 386
Db 63 VTGIVKRLKDDC-ERGLDGFPTTQAQAELEIEYKRPIDYVINIEVDKVL 121
QY 387 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYRNSAD 442
D 387 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYRNSAD 442
Db 122 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYRNSAD 442
QY 443 LEQLY---GSAITLNGDQDPYTFV 463
D 443 LEQLY---GSAITLNGDQDPYTFV 463
Db 182 ILDFYSEKGYLANVNGQDIQDVY 205

RESULT 11

H90019
adenylate kinase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Accession: H90019
R:Auroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90019
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <KUR>
A:Cross-references: UNIPROT:Q9S840; GB:BA000018; PID:g13702029; PIDN:BA843321.1; GSPDB:G13702029; MUID:21311952; PMID:11418146
A:Experimental source: strain N315
C:Genetics:
A:Gene: adk
C:Superfamily: adenylate kinase

Query Match 9.7%; Score 242; DB 2; Length 215;
Best Local Similarity 28.1%; Pred. No. 1.6e-09;
Matches 56; Conservative 48; Mismatches 83; Indels 12; Gaps 4;
QY 271 VLLGPGVSGKSLQAALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPDS 330
D 271 VLLGPGVSGKSLQAALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPDS 330
Db 3 IILMGLPGAGKGTQSEIVKKEPPIPHISTGDMFRAMKEETPLGLEAKSYIDGELVPDE 62
QY 331 LLMKVLSORLDQDCIQKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIM 386
D 331 LLMKVLSORLDQDCIQKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIM 386
Db 63 VTGIVKRLKDDC-ERGLDGFPTTQAQAELEIEYKRPIDYVINIEVDKVL 121
QY 387 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYRNSAD 442
D 387 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYRNSAD 442
Db 122 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYRNSAD 442
QY 443 LEQLY---GSAITLNGDQD 458
D 443 LEQLY---GSAITLNGDQD 458
Db 182 ILDFYDQKGVNLKIDGSKD 200

RESULT 12

B84986
adenylate kinase (EC 2.7.4.3) [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
R:Accession: B84986
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.; Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.?
A:Reference number: B84986; MUID:20445173; PMID:10993077
A:Accession: B84986
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: adk; BU484
C:Superfamily: adenylate kinase
C:Keywords: phosphotransferase

Query Match 9.7%; Score 241.5; DB 2; Length 215;
Best Local Similarity 28.8%; Pred. No. 1.8e-09;
Matches 52; Conservative 44; Mismatches 81; Indels 5; Gaps 2;
QY 270 RVLLGPGVSGKSLQAALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPD 329
D 270 RVLLGPGVSGKSLQAALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPD 329
Db 2 RIILGAPGAGKGTQSEIVKKEPPIPHISTGDMFRAMKEETPLGLEAKSYIDGELVPDE 61
QY 330 LLMKVLSORLDQDCIQKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
D 330 LLMKVLSORLDQDCIQKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
Db 62 EIVCHLTKNRIKKHDCI-NGFILDGFPRTIQALYLSKKNIKIDYVLEFIIPHEYLRI 120
QY 390 TLRRIDPVTGERHYLMYKPPPTMEI---IQARLLQNPDAEQVKLMDLFYRNSADLEQ 445
D 390 TLRRIDPVTGERHYLMYKPPPTMEI---IQARLLQNPDAEQVKLMDLFYRNSADLEQ 445
Db 121 SGRIHQSGRIYHVKKFPKIKDKDDLTTGQTLTKRDKKRGKRLKEKKVHDPLVQ 180
QY 446 LY 447
D 446 LY 447
Db 181 Y 182

RESULT 13

AG0378
adenylate kinase (EC 2.7.4.3) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
R:Accession: AG0378
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N.; Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0378
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-214 <KUR>
A:Cross-references: UNIPROT:O69172; GB:AL590842; PIDN:CAC92354.1; PID:g15981059; GSPDB:G15981059; MUID:21470413; PMID:11586360
A:Genetics:
A:Gene: adk
C:Superfamily: adenylate kinase
C:Keywords: phosphotransferase

Query Match 9.6%; Score 240; DB 2; Length 214;
Best Local Similarity 28.6%; Pred. No. 2.2e-09;
Matches 53; Conservative 46; Mismatches 74; Indels 10; Gaps 4;
QY 59 RVILGPPASGKTTIAMWLCKHNSLLTLENI---LNEFSYTATFARLYLQRTVPS 115
D 59 RVILGPPASGKTTIAMWLCKHNSLLTLENI---LNEFSYTATFARLYLQRTVPS 115
Db 2 RIILGAPGAGKGTQSEIVKKEPPIPHISTGDMFRAMKEETPLGLEAKSYIDGELVPDE 61
QY 116 ALLVQLIERLAEDCIKQWILDGIPETREQALRIQTLGITPRHVIVLSAPDVLIERN 175
D 116 ALLVQLIERLAEDCIKQWILDGIPETREQALRIQTLGITPRHVIVLSAPDVLIERN 175
Db 62 ELVIALVKERITQEDC-RDGLDGFPTTQAQAELEIEYKRPIDYVINIEVDKVL 120
QY 176 LKRRIDPVTGERHYLMYKPPPTMEI---RLMVPEIDISELTAQLLEYHNRVVI 230
D 176 LKRRIDPVTGERHYLMYKPPPTMEI---RLMVPEIDISELTAQLLEYHNRVVI 230
Db 121 VGRVHAASGRVHVKN-PPKVEDKDDVTGELTIKDDQENATVRKRLLEYHQQTAPLV 179
QY 231 PSYPK 235

A;Residues: 1-215 <GLA>
A;Cross-references: UNIPROT:Q927M8; GB:AL592022; PIDN:CA97986.1; PID:gl6415296; GSPDB:GN
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: adk
C;Superfamily: adenylate kinase

Query Match 9.5%; Score 237; DB 2; Length 215;
Best Local Similarity 28.7%; Pred. No. 3.6e-09;
Matches 60; Conservative 50; Mismatches 87; Indels 12; Gaps 5;

QY	270	RVLILGPVSGKSLQAALLAOKYRLVNVCCQLLKEAVADRTTFGELIQPFPEKEMAVPD	329
DB	2	KLVLMGLPGAGKGTQAEQIVKYNIPHISTGDMFRAAMKNNTELGGKAKSPMDNGDLVPD	61
QY	330	SLLMKVLSQRLDQDCIQKGVNLHGVPRLDQA-----HLLNRLGYNPNRVFFLNVPDSI	385
DB	62	EVTNGIVVERLAEDDA-KNGFLLDGFPRTVQABELENIILSDLTGELDAVINIEVDKDL	120
QY	386	MERLTLRIDPVTGERYHLMYKPPPT---MEIQ-ARLLQNPKDAEEQVKLMDLFYRNSA	441
DB	121	MKRLTGRWICRTCGKTYHEIYNPPKVPKCKDLGGELYQREDDKKETVENELNVNMKQTK	180
QY	442	DLEQLY---GSAITLNGDQDPVTTFEYIE	467
DB	181	PLLDIFYSEKGLHSINGEQINDVFDVE	209

Search completed: March 18, 2005, 15:21:33
Job time : 44 secs

Db 180 SYHK 184
RESULT 14
KIHUA3
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human
N;Alternate names: adenylate kinase 3
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A16380; S16381
R;Xu, G.; O'Connell, P.; Stevens, J.; White, R.
Genomics 13, 537-542, 1992
A;Title: Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3
A;Reference number: A42820; MUID:92347846; PMID:1639383
A;Accession: A42820
A;Molecule type: mRNA
A;Residues: 1-223 <XUG>
A;Cross-references: UNIPROT:P27144; EMBL:X60673; NID:G28576; PIDN:CAA43088.1; PID:G28577
A;Experimental source: frontal-cortex
A;Note: Sequence extracted from NCBI backbone (NCBIN:109644, NCBIP:109645)
C;Comment: This isozyme is found in the mitochondrial matrix.
C;Genetics:
A;Gene: GDB:AK3
A;Cross-references: GDB:118988; OMIM:103030
A;Map position: 9pter-9p13
C;Function:
A;Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu
A;Note: GTP is preferred to ATP as a substrate
C;Superfamily: adenylate kinase
C;Keywords: ATP; mitochondrial matrix; mitochondrion; P-loop; phosphotransferase
F;12-19/Region: nucleotide-binding motif A (P-loop) #status atypical
F;85-89/Region: nucleotide-binding motif B #status atypical
F;22,33,58/Active site: Cys, His, Ser, Asp #status predicted

QY	270	RVLILGPVSGKSLQAALLAOKYRLVNVCCQLLKEAVADRTTFGELIQPFPEKEMAVPD	329
DB	7	RAVLIGPGSGKGTVCQRIQNFGLHLSGHFLRENKASTEVGEMAKQYIEKSLLVDP	66
QY	330	SLLMKVLSQRLDQDCIQK--WVLHGVPRLDQHLNRLGYNPNRVFFLNVPDSIME	387
DB	67	HVITRLMWSELEN---RRGQHWLLDGFPTLQGAELDKI-CEYDLVLSLNIPFETLKD	121
QY	388	RUTLRIDPVTGERYHLMYKPPPTMEIQ---ARLLQNPKDAEEQVKLMDLFYRNSADL	443
DB	122	RLSRRWIHPSPGRVYNLDFNPHVHGIDDVTCGEPLVQEDDKPEAVARLRQYKDVAKPV	181
QY	444	EOLYGSATL---NGDQD-----PYTVPEYIESGIINPLPKK	477
DB	182	IELYKSGVHLHQFSGTETNKIWPVYVTLF-----SNKITPIQSK	220

RESULT 15
AB1777
adenylate kinases homolog adk [imported] - Listeria innocua (strain Clp11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1777
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1777
A;Status: preliminary
A;Molecule type: DNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:08:37 ; Search time 181 seconds
(without alignments)
1355.171 Million cell updates/sec

Title: US-10-798-773-2

Perfect score: 2500

Sequence: 1 MDATIAHPRIPEMPQYGE.....YTVPEYIESGIINPLPKIP 479

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	479	2 Q96MA6	Q96ma6 homo sapien
2	2008	80.3	479	2 Q68FP8	Q68fp8 rattus norv
3	1429	57.2	275	2 Q8N9W9	Q8n9w9 homo sapien
4	1409	56.4	485	2 Q6P618	Q6p618 xenopus tro
5	372.5	14.9	290	2 Q6ZC69	Q6zc69 oryza sativ
6	364.5	14.6	283	1 KADD_ARATH	Q9fij7 arabidopsis
7	363.5	14.5	222	1 KADC_MAIZE	P43188 zea mays (m
8	363.5	14.5	260	2 Q6Y8Q6	Q6y8q6 trypanosoma
9	342	13.7	269	2 Q9N910	Q9n910 leishmania
10	333.5	13.3	588	2 Q8VYL1	Q8vyl1 arabidopsis
11	320	12.8	217	2 Q6FY07	Q6fy07 arabidopsis
12	313.5	12.5	260	2 Q6QT32	Q6qt32 trypanosoma
13	292	11.7	221	1 KAD_THETN	Q8v7x4 thermotaneer
14	288	11.5	215	1 KAD_OCEIH	Q8etw3 oceanobacil
15	286	11.4	260	2 Q7YUN3	Q7yun3 trypanosoma
16	281	11.2	212	1 KAD_STRMU	Q8ds33 streptococc
17	279.5	11.2	217	2 Q64AS6	Q64as6 uncultured
18	279	11.2	211	1 KAD_FUSNN	Q8re31 fusobacteri
19	277	11.1	216	1 KAD_CLOTE	Q890q5 clostridium
20	275	11.0	211	2 Q7P5X4	Q7p5x4 fusobacteri
21	274	11.0	217	1 KAD_ARCFU	Q29581 archaeoglob
22	273	10.9	212	1 KAD_STRFN	Q97su1 streptococc
23	272	10.9	212	1 KAD_STRR6	Q8drd4 streptococc
24	272	10.9	210	1 KAD_BACHD	P38372 bacillus ba
25	271	10.8	220	2 Q62HI0	Q62hi0 burkholderi
26	271	10.8	220	2 Q63WL6	Q63wl6 burkholderi
27	268	10.7	219	2 Q6FD71	Q6fd71 acinetobact
28	260	10.4	215	1 KAD_CLOAB	Q37ej9 clostridium
29	260	10.4	216	2 Q73F75	Q73f75 bacillus ce
30	259	10.4	212	1 KAD_STRPY	P82549 streptococc
31	258	10.3	212	1 KAD_STRAS	P65203 streptococc

32 258 10.3 212 1 KAD_STRAS P65204 streptococc
33 258 10.3 212 1 KAD_STRP3 Q8kx1 streptococc
34 258 10.3 212 1 KAD_STRP8 Q9p24 streptococc
35 258 10.3 216 1 KAD_BACCR Q8ij22 bacillus ce
36 258 10.3 218 1 KAD_CLOPE Q8xhu4 clostridium
37 257.5 10.3 214 1 KAD_VIBCH Q9ktb7 vibrio chol
38 257 10.3 216 2 Q67JW4 Q67jw4 symbiobacter
39 257 10.3 220 1 KAD_GLOVI Q7nkt5 symbiobacter
40 256.5 10.3 209 1 KAD_TRYBR Q61069 trypanosoma
41 256.5 10.3 218 1 KAD_BORPE P39068 bordetella
42 255.5 10.2 206 1 KAD_AOUAE Q66490 aquifex aeo
43 255.5 10.2 218 1 KAD_BORBR Q7wku8 bordetella
44 255.5 10.2 218 1 KAD_BORPA Q7wgo bordetella
45 252.5 10.1 214 1 KAD_VIBVU Q8dfmi vibrio vuln

ALIGNMENTS

RESULT 1
ID Q96MA6 PRELIMINARY; PRT; 479 AA.
AC Q96MA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein FLJ32704 (Chromosome 9 open reading frame 98).
DE
GN Name=C9orf98;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC IISUSe-Testis;
RX PubMed=14702039; DOI=10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Iwayanagi T., Wagatsuma M., Shiratori K., Murakami K., Saitsu K., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Murakawa M., Ono Y., Kimata K., Ishihashi T., Yamashita H., Hirakawa M., Tanai H., Kimura K., Ishihashi T., Watanabe M., Hirakawa M., Fujimori K., Kanehori K., Kanehori S., Watanabe M., Hirakawa M., Hotuta T., Ishida S., Togashi S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama K., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirose M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inegaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugeno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., *Complete sequencing and characterization of 21,243 full-length human cDNAs.*; Nat. Genet. 36:40-45 (2004).
[2]
SEQUENCE FROM N.A.
TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the EMBL/GenBank/DBJ databases.
CC EMBL; AK057266; BAB71402.1; -;
CC EMBL; BC034776; AAH34776.1; -;
CC EMBL; BC050576; AAH50576.1; -;
CC HSSP; P43188; 1ZAK.
CC GO; GO:0005524; F-ATP binding; IEA.
CC GO; GO:0008603; F-cAMP-dependent protein kinase regulator act. .; IEA.
CC GO; GO:0016301; F-kinase activity; IEA.
CC GO; GO:0016740; F-transferase activity; IEA.
CC GO; GO:0007165; P-signal transduction; IEA.
CC InterPro; IPR000850; Adenylate_kin.
CC InterPro; IPR003117; Rila.
CC Pfam; PF00406; ADK; 1.
CC PRINTS; PR00094; ADENYLTKNASE.
CC ProDom; PD000657; Adenylate_kin; 1.
CC Kinase; Transferase.
CC SEQUENCE 479 AA; 54925 MW; 9E4EABA3F429B731 CRC64;
Query Match 100.0%; Score 2500; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 3.9e-155; Indels 0; Gaps 0;
Matches 479; Conservative 0; Mismatches 0;
QY 1 MDATIAPHRIPEMPQGEENHIFELMQLNLEQLIHQPEDPIPFMIQHLHRDNDVPRI 60
DB 1 MDATIAPHRIPEMPQGEENHIFELMQLNLEQLIHQPEDPIPFMIQHLHRDNDVPRI 60
QY 61 VILGPPASGKTTIAMWLCCKHNSLLTLENLIINEFSYATARRLYLQKTVPSALLVQ 120
DB 61 VILGPPASGKTTIAMWLCCKHNSLLTLENLIINEFSYATARRLYLQKTVPSALLVQ 120
QY 121 LIQRLAEEDCIKQWILDGIPETREOALRIQTLGTPRHVIVLSAPDVLIERNLGKRI 180
DB 121 LIQRLAEEDCIKQWILDGIPETREOALRIQTLGTPRHVIVLSAPDVLIERNLGKRI 180
QY 181 DPQTGEYHTTFDWPPESEIQNLNMPVEDISELTAQKLLLEYHRNIVRVPKILKVI 240
DB 181 DPQTGEYHTTFDWPPESEIQNLNMPVEDISELTAQKLLLEYHRNIVRVPKILKVI 240
QY 241 SADQPCVDVFTYQALTYVQSNHRTNAPETPRVLLGPGVSGSKSQALLAQKYLNVNCCG 300
DB 241 SADQPCVDVFTYQALTYVQSNHRTNAPETPRVLLGPGVSGSKSQALLAQKYLNVNCCG 300
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQLDQDDCIQKGVWLHGVPRDLD 360

301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQLDQDDCIQKGVWLHGVPRDLD 360
361 QAHLLNRLGYNPNRVFFLNVPDPSIMERLTTLRRIDPVTGVRHLMYKPPPTWEIQARLIQ 420
361 QAHLLNRLGYNPNRVFFLNVPDPSIMERLTTLRRIDPVTGVRHLMYKPPPTWEIQARLIQ 420
421 NPKDAEQVKLQMDLFRNSADLEQLYGSNITLNGDQDPTVTFEYIESGIINPLPKKIP 479
421 NPKDAEQVKLQMDLFRNSADLEQLYGSNITLNGDQDPTVTFEYIESGIINPLPKKIP 479

RESULT 2
Q68FP8 PRELIMINARY; PRT; 479 AA.
AC Q68FP8; 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein MGC94995.
GN Name=MGC94995;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC TISSUE=Testis;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC EMBL; BC079446; AAH79446.1; -;
CC InterPro; IPR000850; Adenylate_kin.
CC Pfam; PF00406; ADK; 1.
CC PRINTS; PR00094; ADENYLTKNASE.
CC ProDom; PD000657; Adenylate_kin; 1.
CC Hypothetical protein; Kinase; Transferase.
CC SEQUENCE 479 AA; 54965 MW; D2331D51EFC5A15A CRC64;
Query Match 80.3%; Score 2008; DB 2; Length 479;
Best Local Similarity 77.0%; Pred. No. 5.4e-123; Indels 0; Gaps 0;
Matches 368; Conservative 57; Mismatches 53;
QY 1 MDATIAPHRIPEMPQGEENHIFELMQLNLEQLIHQPEDPIPFMIQHLHRDNDVPRI 60
DB 1 MDATSAPRIPEMPQGEYHIFEMQSMLEQLIHQPEDPIFSMTSLRRNDNVPRI 60
QY 61 VILGPPASGKTTIAMWLCCKHNSLLTLENLIINEFSYATARRLYLQKTVPSALLVQ 120
DB 61 VILGPPASGKTTIAMWLCCKHNSLLTLENLIINEFSYATARRLYLQKTVPSALLVQ 120

CC 121 LIOERLAEDCIKQWILGDPETREOALRIQTLGTPRHVIVLSAPDVLIERNLGKRI 180
DR EMBL: AK093446; BAC04168.1; -
DR HSP: P43188; 1ZAK.
DR GO: CO:0005524; F:ATP binding; IEA.
DR GO: CO:0016301; F:kinase activity; IEA.
DR GO: CO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; ADK; 1.
DR PRINTS: PR00094; ADENYLTKNASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR Kinase; Transferase.
SQ SEQUENCE 275 AA; 31455 MW; B90C76CF137D6C34 CRC64;

Query Match 57.2%; Score 1429; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 MYPEDISELTAQKLLHYHNRIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 264
Db 1 MYPEDISELTAQKLLHYHNRIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 60

QY 265 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTIGELIQPFPEKE 324
Db 61 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTIGELIQPFPEKE 120

QY 325 MAVPDSLLMKVLSQRLDQDCIQKGVNLHGVPRDLDOAHLLNRLGYNRNVFLNVPFDS 384
Db 121 MAVPDSLLMKVLSQRLDQDCIQKGVNLHGVPRDLDOAHLLNRLGYNRNVFLNVPFDS 180

QY 385 IMERLTLRRIDPVTGERVHLYKPPPTMETQARLLQNPXDABEQVKLQMDLFPYNSADLE 444
Db 181 IMERLTLRRIDPVTGERVHLYKPPPTMETQARLLQNPXDABEQVKLQMDLFPYNSADLE 240

QY 445 QLVGSAITLNGDDPYTVFVYIESGIINPLPKIP 479
Db 241 QLVGSAITLNGDDPYTVFVYIESGIINPLPKIP 275

RESULT 3

Q8N9W9 PRELIMINARY; PRT; 275 AA.
AC Q8N9W9;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ36127.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Testis;
RP Med14702039; DOI=10.1038/ng1285;
RX Ota T., Suzuki Y., Nishikawa T., Ohtsuka T., Sugiyama T., Irie R.,
RA Nakagawa S., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takehashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Muesashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Wakakami T., Noguchi S., Itoh T., Shigetani K., Senaki M.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Shirai Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh N., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Okumura K., Nagase T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs." Nat. Genet. 36:40-45(2004).

-1- SIMILARITY: Belongs to the adenylate kinase family.
CC EMBL: AK093446; BAC04168.1; -
DR HSP: P43188; 1ZAK.
DR GO: CO:0005524; F:ATP binding; IEA.
DR GO: CO:0016301; F:kinase activity; IEA.
DR GO: CO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; ADK; 1.
DR PRINTS: PR00094; ADENYLTKNASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR Kinase; Transferase.
SQ SEQUENCE 275 AA; 31455 MW; B90C76CF137D6C34 CRC64;

Query Match 57.2%; Score 1429; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 MYPEDISELTAQKLLHYHNRIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 264
Db 1 MYPEDISELTAQKLLHYHNRIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 60

QY 265 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTIGELIQPFPEKE 324
Db 61 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTIGELIQPFPEKE 120

QY 325 MAVPDSLLMKVLSQRLDQDCIQKGVNLHGVPRDLDOAHLLNRLGYNRNVFLNVPFDS 384
Db 121 MAVPDSLLMKVLSQRLDQDCIQKGVNLHGVPRDLDOAHLLNRLGYNRNVFLNVPFDS 180

QY 385 IMERLTLRRIDPVTGERVHLYKPPPTMETQARLLQNPXDABEQVKLQMDLFPYNSADLE 444
Db 181 IMERLTLRRIDPVTGERVHLYKPPPTMETQARLLQNPXDABEQVKLQMDLFPYNSADLE 240

QY 445 QLVGSAITLNGDDPYTVFVYIESGIINPLPKIP 479
Db 241 QLVGSAITLNGDDPYTVFVYIESGIINPLPKIP 275

RESULT 4
Q8P618 PRELIMINARY; PRT; 485 AA.
AC Q8P618;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76170.
GN Name=MGC76170;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RC TISSUE=Embryo;
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worsley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton J., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Embryo;

Klein S., Gerhard D.S.; RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

CC -I- SIMILARITY: Belongs to the adenylyate kinase family.

EMBL; BC062516; AAH62516.1; -.

HSSP; P05082; 1AKE.

DR GO: 0005524; F:ATP binding; IEA.

DR GO: 0008603; F:AMP-dependent protein kinase regulator act. .; IEA.

DR GO: 0007165; P:signal transduction; IEA.

DR GO: 0007165; P:signal transduction; IEA.

DR InterPro: IPR000850; Adenylyate_kin.

DR InterPro: IPR003117; RIIa.

DR Pfam: PF00406; ADK; 2.

DR PRINTS; PR00094; ADENYLTKINASE.

DR ProDom; PD000657; Adenylyate_kin; 2.

KW Hypothetical protein; Kinase; Transferase.

SEQUENCE 485 AA; 54786 MW; C2810A7C1EBBAD6C CRC64;

Query Match 56.4%; Score 1409; DB 2; Length 485;

Best Local Similarity 54.1%; 98; Pred. No. 7.5e-84;

Matches 259; Conservative 122; Indels 0; Gaps 0;

QY 1 MDATIAPIRIPPENPOYGEENHIFELMQNMLEQLLIHQEPDIPPMIQLHRLNDNVPRI 60

DB 1 MDATRKPLRIIPAMALYAEQGVFDIIQKMWKLVLDVRPKDPIQYIMDHLSNDDNDDVPRV 60

QY 61 VILGPPASGKTTIAMWLCKHLNSSLTLENILNFEFSYTAEARRLYLQRTVPSALLVQ 120

DB 61 FILGPPASGKHTMAKLLCRNLNATHLTPESVLSSDVSLAKEAQSRYDKQGVDPDELWAK 120

QY 121 LIQRLABEDCIKQWILDGIPETREQALRIQTGITPRHVIVLSAPDVLIERNLGKRI 180

DB 121 LMQRLSKVDCKIKRGWILEGPPKREQALQLMAGICPDHLVLDAPDIVLIERNMGKRI 180

QY 181 DPQCEIYHTTVDWPESEIQNRLMVPRDISELETAQKLEVHRNIVRIVPSIKLVKI 240

DB 181 DTANGEVYHTTFDWPSPDPTQVNLVPEPGISEEFTGLRIEVRNIPGILATYPTKTSKI 240

QY 241 SADQPCVDVIFYQALTYVQSNHRTNAPFTVRVLLLPVSGSKSLQALLAOKVRLVNVCCG 300

DB 241 NADQFVMDVFSQVLTIFVLISKPSLAPHTPRILLYGPPGSGRSLQASLLAQKYGIVNICG 300

QY 301 QLLKEAVDRTTFGELIOPFFKEWAVPDSLMLKVLRSORLQDQCICQKGWVLHGVPRLD 360

DB 301 QVLKEAVADQTKLGEVIQIYENDQQVDPNLVILKILTEHLSLESATHGWVLHGFPDRTD 360

QY 361 QAHLNRLGYNPNRVFFLNVPPDSIMERLITLRRIDPVTGERVHLMKPPPTMEIQARLIQ 420

DB 361 QAALLKADAGFVNPVFSLDLSDVVIERLSLCWMTDPVSGERYHDYIKPAPSEVHERLQQ 420

QY 421 NPKDAEQVKLMOLFYNRSADLEQLYGSAILTNGQDQVTFVFEYESGIIINPLPKPI 479

DB 421 NPRHSQRQVRLQMDMYHANAELDEFTYDPVHINADQDPTVFEFIESYTVSPPLPLP 479

RESULT 5

Q6ZC69 PRELIMINARY; PRT; 290 AA.

AC Q6ZC69

DT 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE Putative adenylyate kinase, chloroplast (ATP-AMP transphosphorylase).

DE Name=E0007D08.12;

OS Oryza sativa (Japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yanada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anari Y.,
RA Arakawa T., Barth J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koessena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tames R., Vayenberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome.";
RL Science 302:842-846 (2003).
CC -!- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC -!- SIMILARITY: Belongs to the adenylate kinase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB016886; BAB11331.1; -;
DR EMBL; AY049305; AAK83647.1; -;
DR EMBL; E1001036; AAN46790.1; -;
DR HSP; P43188; 12AK.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR PRODOM; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW ATP-binding; Chloroplast; Kinase; Transferase; Transit peptide.
FT CHAIN 1 59 Chloroplast (potential).
FT NP_BIND 60 283 Probable adenylate kinase 2.
FT NP_BIND 71 79 ATP (By similarity).
SQ SEQUENCE 283 AA; 31452 MW; 1461D1A36F2DF4E9 CRC64;
Query Match 14.6%; Score 364.5; DB 1; Length 283;
Best Local Similarity 36.4%; Pred. No. 6.4e-16;
Matches 76; Conservative 39; Mismatches 93; Indels 1; Gaps 1;
QY 270 RVLLGPGVSGSLQAALLAOKYRLVNVCGQLKEAVADRTTFGELIQPFKEKMAVDP 329
DB 66 KIMISGAPASGKGTQCELLTHYGLVHISAGDLLRAEIASGSENGRRAKEHKGQLVDP 125
QY 330 SLAMKVLSQLDQDCIOKGWLVHGVPRDLQAHNLRLGYNPNKRVFELNVFDFSI MERL 389
DB 126 EIVVMVAVKRLSDTSEQSGWLLDGYPRASQATKLGFGQPDLFIVLEVPBEILIERV 185
QY 390 TLRRIDPVTGTERHYMKPPPTMEIQARLQNPDAEQVKLMDLFRNSADLEOLYGS 449
DB 186 VGRRLDPVTKYIHLKSPETETIAVRLTQRPDDETEKAKLRLKTHNQNSVDLSYDD 245
QY 450 -AITLNGDQDPVTVFVIESGIINPLPKK 477
DB 246 ITIKIEGRNKEEVEFAQIDGSLSELLQER 274
RESULT 7
KADC_MAIZE
ID_KADC_MAIZE STANDARD; PRT; 222 AA.

P43188;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Adenylate kinase, chloroplast (EC 2.7.4.3) (ATP-AMP
transphosphorylase).
Name=ADKI;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
[1] SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Leaf;
RX MEDLINE=94298837; PubMed=8026505;
RA Schiltz E., Burger S., Grafmuller R., Deppert W.R., Haehnel W.,
RT "Primary structure of maize chloroplast adenylate kinase.";
RL Eur. J. Biochem. 222:949-954 (1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=98089957; PubMed=9428681;
RA Wild K., Grafmuller R., Wagner E., Schulz G.B.;
RT "Structure, catalysis and supramolecular assembly of adenylate kinase
from maize.";
RL Eur. J. Biochem. 250:326-331 (1997).
CC -!- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth. The maize enzyme also works with CMP,
CC albeit with 10% of the activity with AMP.
CC -!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- MASS SPECTROMETRY: MW=24867; METHOD=Electrospray; RANGE=1-222;
CC -!- NOTES=Ref.1.
CC -!- SIMILARITY: Belongs to the adenylate kinase family.
DR PIR; S45634; S45634.
DR PDB; 1ZAK; X-ray; A/B=1-222.
DR MaizeDB; 13836; -.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR PRODOM; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW 3D-structure; ATP-binding; Chloroplast; Direct protein sequencing;
KW Kinase; Transferase.
FT NP_BIND 12 20 ATP (By similarity).
FT STRAND 8 12
FT TURN 14 15
FT HELIX 18 29
FT STRAND 32 33
FT HELIX 36 46
FT TURN 47 47
FT HELIX 49 59
FT TURN 60 61
FT HELIX 66 78
FT TURN 80 84
FT HELIX 85 95
FT TURN 97 90
FT STRAND 96 103
FT TURN 104 106
FT STRAND 111 116
FT HELIX 119 126
FT TURN 127 128
FT STRAND 129 131
FT TURN 133 135
FT STRAND 138 140
FT TURN 150 154
FT HELIX 156 156
FT STRAND 159 160
FT TURN 163 164
FT HELIX 165 165

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FT TURN 183 184
FT STRAND 188 192
FT HELIX 197 219
FT TURN 220 220
SQ SEQUENCE 222 AA; 24867 MW; 19257324F8B7630D CRC64;

Query Match 14.5%; Score 363.5; DB 1; Length 222;
Best Local Similarity 37.3%; Pred. No. 5.5e-16;
Matches 78; Conservative 40; Mismatches 90; Indels 1; Gaps 1;

Qy 270 RVLLGPGVSGKSLQALLAQKYLNVNCGQLLKEAVADRITFGELIQFFFEKEMAVPD 329
Db 7 KWMISGAPAGKGTQCELIKTQKLAHISAGDILRAEIAAGSENGKRAKEFMEKGLVDP 66

Qy 330 SLMKVLSQRLDQDCIQKGVNLGVPRDLDDQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
Db 67 EIVNVNMYKRLRQPDAGENGWLLDGYPRSYQMALETLEIRPDTFILLDVPDELLVERV 126

Qy 390 TLRIDPVTGRIYHLMKPPPTMEIQARLLQNPDKADEQVKLMDLFRNSADLEQLYGS 449
Db 127 VGRLLDPVTGRIYHLMKPPPTMEIQARLLQNPDKADEQVKLMDLFRNSADLEQLYGS 186

Qy 450 AIT-LNGDQDPVTVFETIESGIINPLPKK 477
Db 187 IIVKQGDATVDANFAKIDELLSILEKK 215

RESULT 8
Q6Y8Q6 PRELIMINARY; PRT; 260 AA.
AC Q6Y8Q6;
DT 05-JUL-2004 (TREMREL. 27, Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 05-JUL-2004 (TREMREL. 27, Last annotation update)
DE Adenylate kinase.
GN Name=AdeK1;
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL Brenner;
RA Bouvier L.A., Miranda M.R., Canepa G.E., Pereira C.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; A169824; RA013019.1; -.
DR HSSP; P05082; IAKE.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR007862; ADK_lid.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR PRODOM; PD000657; Adenylate kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
DR KINASE; Transferase.
SQ SEQUENCE 260 AA; 29337 MW; BCB888E43115F8C CRC64;

Query Match 14.5%; Score 363.5; DB 2; Length 260;
Best Local Similarity 30.6%; Pred. No. 6.7e-16;
Matches 82; Conservative 53; Mismatches 106; Indels 27; Gaps 5;

Qy 200 IQNRLMVPDISELETAQKLEHYNIRVIPSVPKILKVISADQPCVDVQALRYVQS 259
Db 5 LDNKL---EYLQKNIQAQLTEHIVRNIMEDLPENP-----IKV--- 40

Qy 260 NHRTNAPTPRVLGPGVSGKSLQALLAQKYLNVNCGQLLKEAVADRITFGELIQ 319
Db 5 LDNKL---EYLQKNIQAQLTEHIVRNIMEDLPENP-----IKV--- 40

41 HDLLERPIPIQIVIAGPPGSGKGTQCAIVERGVVHSSGDLRLRAEVAAGTEVGMAET 100
320 FFEKEMAVPDSLLMKVLSQRLDQDCIQKGVNLGVPRDLDDQAHLLNRLGYNPNRVFFLN 379
101 FIHNGENVFNKIVISAVRKELEQDDVKGWLLDGFPRSQDQAEALLESSGIVPHVFLLE 160
380 VPFDSIMERLTLRIDPVTGRIYHLMKPPPTMEIQARLLQNPDKADEQVKLMDLFRN 437
161 VPDITVVERIENRRTDPAITGMVYHLLYNPPPPEDVALCERLIQDQDDHRETVEARLIYH 220
438 RNSADLEQLYGSAL-TLNGDQDPVTVE 464
221 EKLHGLKEHYGTLVETTINGDSIHAVTE 248

RESULT 9
Q9N910 PRELIMINARY; PRT; 269 AA.
AC Q9N910;
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Possible adenylate kinase.
GN Name=L6294.05;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,
RA Quail M., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; AL354533; CAB89615.1; -.
DR HSSP; P43188; 1ZAK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000850; Adenyl_kin_sub.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
DR KINASE; Transferase.
SQ SEQUENCE 269 AA; 30060 MW; BAB58834D6984E1 CRC64;

Query Match 13.7%; Score 342; DB 2; Length 269;
Best Local Similarity 31.3%; Pred. No. 1.8e-14;
Matches 81; Conservative 54; Mismatches 104; Indels 20; Gaps 6;

Qy 17 YGEENHIFELMQNMLEQLLIHQEPDIPFMQLHRLDNDNVPRIVLGPPASGKTTIAMW 76
Db 14 YIKDNNIGQLMEYILRCIITDKPKTPLYV--HELTASPLPPRVVLGASGKGTQARH 71
77 LCK-----HLNS-SILLTLENILNEFSYATETEARLYLQRTKTVPSALLVQLIOE 124
72 ICSTYKKAIGKPKVHVSGLLRAE---VAQTHLGKIAENFMQRGBELVDSLIISIRN 128
125 FLAEDCTKCGWLLDGPETREQALRIQTIGIPRHVIVLSAPDTVLIERNLGKRIDPOT 184
129 RLTDQDAVWNGWLLDGFPRTRSQALDAAGLCPRIFVLDTPDDVLFGVREGRTDPT 188

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QY 185 GBHYHTFDWPESE--IQNLMVPEDISELETAQKLEHVRNIVRIPSPKILKVISA 242
Db 189 GIIYHLKNTPPENDTALLERQHRDDDTREVLGRLETHYSMVGEGLDYGSIMYHVDG 248
QY 243 DQPCVDVFOYQALTYVQSNH 261
Db 249 NRPEAAITKDITEYLQ-NH 266

RESULT 10
QSVYL1 PRELIMINARY; PRT; 588 AA.
AC QSVYL1;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 05-JUL-2004 (TRENBLrel. 20, Last sequence update)
DE Putative adenylyate kinase.
GN Name=At5g35170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Huan V.W.,
RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wu H.C., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the adenylyate kinase family.
DR EMBL; AI070456; AA049559.1; -.
DR EMBL; AY133763; AAM91697.1; -.
DR HSSP; P43188; 1ZAK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR PRODOM; PD000657; Adenylyate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 588 AA; 65738 MW; 3AA0B81ABFC4B62B CRC64;

Query Match 13.3%; Score 333.5; DB 2; Length 588;
Best Local Similarity 33.7%; Pred. No. 1.7e-13;
Matches 68; Conservative 47; Mismatches 84; Indels 3; Gaps 2;

QY 264 NAPPFPRVLLGPGSGKSLQALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKEK 323
Db 77 NEPL--KVMISGAPASGKGTCCELIVHKFGLVHISTGDLRAEVSSGTDIGKRAKEFVNS 134

QY 324 ENAVPDSLLMKVLSQRDQDCIQKGWLVHGVPRDLQAHLLNRLGYNPNRVFFLNVPFD 383
Db 135 GSLVDPDEIVTAMVAGRLSREDAKEHGWLDDGFPSPFAQSLDKLVNKPDIIFILLDVPDE 194
QY 384 SIMERLTLRRIDPVTGERVHLMYKPPPTWEIQARLLQNPKDAEQVKLWDLFYNSADL 443

RESULT 11
QSVY07 PRELIMINARY; PRT; 217 AA.
AC QSVY07;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Adenylyate kinase-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the adenylyate kinase family.
DR EMBL; AP000421; BAB10023.1; -.
DR HSSP; P43188; 1ZAK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000850; Adenylyate_kin.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR PRODOM; PD000657; Adenylyate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 217 AA; 24065 MW; 76FBED1964ACD04E CRC64;

Query Match 12.8%; Score 320; DB 2; Length 217;
Best Local Similarity 34.4%; Pred. No. 3.7e-13;
Matches 62; Conservative 42; Mismatches 76; Indels 0; Gaps 0;

QY 272 LLLGPGVSGKSLQALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKEKMAVPDSL 331
Db 1 MISGAPASGKGTCCELIVHKFGLVHISTGDLRAEVSSGTDIGKRAKEFVNSGSLVPEI 60

QY 332 LMKVLSQRDQDCIQKGWLVHGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERLTL 391
Db 61 VTAMVAGRLSREDAKEHGWLDDGFPSPFAQSLDKLVNKPDIIFILLDVPDEILDRCVG 120

QY 392 BRIDPVTGERVHLMYKPPPTWEIQARLLQNPKDAEQVKLWDLFYNSADLQYCSAI 451
Db 121 RLRLDPVTGKIYHKNYPPESEDEIKARLVTRPDDTEEKVKARLIQYKQNSEAI 180

RESULT 12
QSVT32 PRELIMINARY; PRT; 260 AA.
AC QSVT32;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Adenylyate kinase 4.
GN Name=Adk4;
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
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Mon Mar 21 09:11:08 2005

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RC STRAIN=CL Brenner;
RA Bouvier L.A., Miranda M.R., Canepa G.E., Pereira C.A.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC EMBL; AY526734; AAS20418.1; -.
DR HSSP; P05082; IAKE.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
KW Kinase; Transferase.
SQ SEQUENCE 260 AA; 29610 MW; OCCAG7290386081F CRC64;

Query Match 12.5%; Score 313.5; DB 2; Length 260;
Best Local Similarity 30.2%; Pred. No. 1.2e-12;
Matches 73; Conservative 52; Mismatches 108; Indels 9; Gaps 5;

QY 17 YGEENHIFELMQLLEQLIHOPEDPPIFMIOHLHRDNVPRIVILGPPASGKTTIAMW 76
DB 13 YFEKHINTLEELPHDVMVHLDDPLQLHAL--DRKTTLRMLVWLGSGAGKRTQSR 70

QY 77 LCKHLNSSLLENLILNEFSYATARR--YLQRTVPSALLVQLIQERLAEDCIK 133
DB 71 IAKGVAVVNVADDFREMSKETKEGVANCMREGIPVPHDVASSELLIRRLKMEDANS 130

QY 134 QGWILDGIPETREQALRIQTLGITPRHVIVLSADPTVLIERNLGRDPQTGEIYHTTFD 193
DB 131 NGWLVNGFRTSEALRQTAGISPLFTILLDLPYENAVQRCNGRRYDPIITQNYHMEFC 190

QY 194 WPESIQNRMLVPED-ISELETAQKLEYHNRIVRVPSPKILKVISADQPCVDVIFYQ 252
DB 191 PPPEGNAVERMFEDDDSLAASVSRWRYFDARKD--ELIECEPVPVRIDGNRP-VDVVSQ 247

QY 253 AL 254
DB 248 EI 249

RESULT 13
KAD THETN STANDARD; PRT; 221 AA.
AC Q8R7X4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN Name=adk; OrderedLocuNames=TTE2271;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen K., Wang J., Yu J., Yang H.;
RA "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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CC -----
DR EMBL; AE013171; AM25415.1; -.
DR HSSP; P27142; IZIN.
DR HAMAP; MF 00235; -.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR000850; Adenylate_kin.
DR InterPro; IPR007862; ADK_lid.
DR Pfam; PF00406; ADK; 1.
DR Pfam; PF05191; ADK_lid; 1.
DR PRINTS; PR00094; ADENYLKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW ATP-binding; Complete proteome; Kinase; Transferase.
FT NP_BIND 7 15 ATP (By similarity).
FT SEQUENCE 221 AA; 25031 MW; B19D5675CE8B33E7 CRC64;

Query Match 11.7%; Score 292; DB 1; Length 221;
Best Local Similarity 28.6%; Pred. No. 2.6e-11;
Matches 61; Conservative 61; Mismatches 79; Indels 12; Gaps 4;

QY 270 RVLLIGPVSGSKLQAALLAOKYRLVNVCCQLLKEAVADRTTFGLIQPFPEKEMAVPD 329
DB 2 RVLLIGPVSGAGGTQLAKIKEFDIPHISTGDIIFQNLRDNTLGLKLAKEYMDKGLLVPD 61

QY 330 SLIMKVLSQLDQDCIOQGVNLHGVPRLDLOAHLNRL-----GYNPNRVFFLAVPDSI 385
DB 62 EVTNRIREDLEKEDC-KKGFLLDGYPNIPQAEELDFLEERGHSLTAVANIQVERAL 120

QY 386 MERLTLRIDPTGYRHYLMYKPPPTMEI-----QARLLQNPQDAEEQVKLQKDLFYRNSA 441
DB 121 IDRITGRRVPCVGATYHIKTSPPKVDNVCDCGSELQSRDDKLESVVKLEVVYKETK 180

QY 442 DLEQLY---GSAITLNGDQDPYTVFYEIESGII 471
DB 181 PLIDYTKGILVNIIDGNKSIDVEFDIKALL 213

RESULT 14
KAD OCEIH STANDARD; PRT; 215 AA.
AC Q8ETW3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN Name=adk; OrderedLocuNames=OB0140;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RA "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RA Ridge and its unexpected adaptive capabilities to extreme
RA environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
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CC or send an email to license@isb-sib.ch).

DR EMBL; AP004593; BAC12096.1; -
DR HSSP; P27143; IZIN.
DR HAMAP; MF_06735; 1.
DR InterPro; IPR000850; Adenylate_kin.
DR InterPro; IPR006259; Adenylate_kin_sub.
DR InterPro; IPR007862; ADK_lid.
DR Pfam; PF00406; ADK; 1.
DR Pfam; PF05151; ADK; 1.
DR PRINTS; PF00094; ADENYL_KINASE.
DR PROSITE; PS00657; Adenylate_kin; 1.
DR PROSITE; PS00135; adk; 1.
DR PROSITE; PS00135; ADENYLATE_KINASE; 1.
KW ATP-binding; Complete proteome; Kinase; Transferase.
FT NE-BIND 7 15
SQ SEQUENCE 215 AA; 24064 MW; 14DEFCC27364E03 CRC64;

Query Match 11.5%; Score 288; DB 1; Length 215;
Best Local Similarity 33.0%; Pred. No. 4.5e-11;
Matches 69; Conservative 46; Mismatches 82; Indels 12; Gaps 4;
QY 271 VLLGPGVSGKSLQAALLAOKYRLVNVCCGQLLKEAVADRTTFGELIQPFKEKEMAVPDS 330
DB 3 LILMLPGAGKGTQAAKINEKYNIPHISTGDMFLRAIKETGELCKAKFMDGDLVPDE 62
QY 331 LLMKVLSQLDQDCIQKGMVLHGVPRLDQA---HLNRLGYNPNRVFFLNVPDSTM 386
DB 63 VTGVIVKERLAMDCC-ANGFLDGFPTTRQAEELQNLSDLGKSIDYVHVDVPEKLV 121
QY 387 ERLTLRRIDPVTGERYHLMYKPPPTMEI---QARLLQNKDAEQVKLMDLFYNSAD 442
DB 122 ERLTGRICPTCGTAYHVYVNPPEKSGICDKGSLQIQDDQDPETVKNRLAVNIEQTP 181
QY 443 LEQLY---GSAITLNGDDPPTVFEVIES 468
DB 182 LLDFFQDKGYLVKVGNGDRDINNVFQDIES 210

RESULT 15

Q7YUN3 PRELIMINARY; PRT; 260 AA.
ID Q7YUN3
AC Q7YUN3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Adenylate kinase.
GN ORFNames=TB927.2.5660;
OS Trypanosoma brucei
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2789169; PubMed=12907728; DOI=10.1093/nar/gkg673;
RA El-Sayed N.M.A.; Ghedin E.; Song J.; MacLeod A.; Bringaud F.;
RA Larkin C.; Haniss D.; Peterson J.; Hou L.; Taylor S.; Tweedie A.;
RA Blandin G.; Khatek H.G.; Lin X.; Mason T.; Hannick L.; Caler E.;
RA Van Aken S.; Bartholomeu D.; Simpson A.J.; Kaul S.; Zhao H.; Pai G.;
RA Gerard C.; Uterback T.; Haas B.; Koo H.I.; Umayam L.; Suh B.;
RA Szabad C.; Leach V.; Qi R.; Zhou S.; Schwartz D.; Feldblyum T.;
RA Adams S.; Tait A.; Turner M.R.; Ullu E.; White O.; Melville S.;
RA Adams M.B.; Fraser C.M.; Donelson J.E.;
RT The sequence and analysis of Trypanosoma brucei chromosome II.;
RT Nucleic Acids Res. 31:4856-4863(2003).
CC [1]-SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; AE017170; AAQ16024.1; -
DR HSSP; P05082; IE4Y.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; ADK; 1.
DR ProDom; PD000657; Adenylate_kin; 1.
KW Kinase; Transferase.
SQ SEQUENCE 260 AA; 29339 MW; 8F15B485E68B1FC7 CRC64;
Query Match 11.4%; Score 286; DB 2; Length 260;
Best Local Similarity 27.2%; Pred. No. 7.8e-11;
Matches 67; Conservative 51; Mismatches 116; Indels 12; Gaps 4;
QY 233 YPKLLKVISADOPCVDFVFOALTYVQSNIHRTNAPTPTRVLLGPGVSGKSLQAALLAOKY 292
DB 21 FEQIVQNIISDAP-----ERPMSYIGDLMRRGIPL--QIFTAGPAGSGKRTQCKNTADRL 73
QY 293 RLNVNCCGQLLKEAVADRTTFGELIQPFKEKEMAVPDSLLMKVLSQRLDQDCIQKGMVL 352
DB 74 GVVLISGQVLTGREGSGSETSQLAHSYVSRGERVPDTLVSMIMKDLRSLQSDAREKGMVL 133
QY 353 HGVPRLDQAHLNRLGYNPNRVFFLNVPDSTMERLTLLRRIDPVTGERYHLMYKPPPTM 412
DB 134 EGYPRNAQQAQAEVEGCVIPQVFIILLDPEDLSFRLEHRRYDPATNKSYHMLNDNPPAE 193
QY 413 EIQ--ARLLQNKDAEQVKLMDLFYNSADLEQLYGSATLNGDDPPTVFEVIESGI 470
DB 194 DVALCERLVORDADPFHESIAKLAQYIESIEGVKKHLGAVIEV---VDARKSVEDVERDI 250
QY 471 INPLPK 476
DB 251 LAAVEK 256

Search completed: March 18, 2005, 15:20:44
Job time : 183 secs

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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:11:03 ; Search time 49 Seconds
(without alignments)
729.733 Million cell updates/sec

Title: US-10-798-773-2
Perfect score: 2500
Sequence: 1 MDATIAPHRIPPEMPQYGE...YTVFEYIESGIINLPKIP 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgm2_6/ptodata/1/aaa/5B.COMB.pap.*
3: /cgm2_6/ptodata/1/aaa/5A.COMB.pap.*
4: /cgm2_6/ptodata/1/aaa/5B.COMB.pap.*
5: /cgm2_6/ptodata/1/aaa/PCTUS.COMB.pap.*
6: /cgm2_6/ptodata/1/aaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	479	4	US-10-141-634-2
2	491	19.6	94	4	Sequence 2, Appli
3	280.5	11.2	222	4	Sequence 4, Appli
4	273	10.9	212	4	Sequence 5675, Ap
5	273	10.9	216	4	Sequence 4124, Ap
6	249	10.0	66	4	Sequence 4765, Ap
7	247.5	9.9	222	3	Sequence 7572, Ap
8	242.5	9.7	215	4	Sequence 3289, Ap
9	240	9.6	223	2	Sequence 1580, Ap
10	240	9.6	223	3	Sequence 5, Appli
11	240	9.6	223	3	Sequence 5, Appli
12	238	9.5	225	4	Sequence 9245, Ap
13	236.5	9.5	223	4	Sequence 12712, A
14	233.5	9.3	227	4	Sequence 7057, Ap
15	233.5	9.3	227	3	Sequence 3, Appli
16	233	9.3	282	4	Sequence 21097, A
17	231.5	9.3	227	4	Sequence 377, App
18	228.5	9.1	227	2	Sequence 1, Appli
19	228.5	9.1	227	3	Sequence 1, Appli
20	225.5	9.0	179	4	Sequence 3142, Ap
21	220.5	8.8	227	2	Sequence 4, Appli
22	220.5	8.8	227	3	Sequence 4, Appli
23	214.5	8.6	240	4	Sequence 5802, Ap
24	212	8.5	237	4	Sequence 10565, A
25	212	8.5	237	4	Sequence 10565, A
26	208.5	8.3	217	4	Sequence 246, App
27	198.5	7.9	231	4	Sequence 3675, Ap

ALIGNMENTS

RESULT 1
US-10-141-634-2
; Sequence 2, Application US/10141634
; Patent No. 6734010
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qionghu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walker, D. Wade
; TITLE OF INVENTION: No. 6734010el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141.634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-141-634-2

Query Match	100.0%;	Score 2500;	DB 4;	Length 479;
Best Local Similarity	100.0%;	Pred. No. 4.4e-251;		
Matches 479;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MDATIAPHRIPPEMPQYGEENHIFELMQLIHQPEDDIPPMIQLHHRDNDNVPI	60	
Db	1	MDATIAPHRIPPEMPQYGEENHIFELMQLIHQPEDDIPPMIQLHHRDNDNVPI	60	
Qy	61	VILGPPASGKTTIAMWLCKHNSLLTLENLINESFSYATARELYLQKTVPSALLVQ	120	
Db	61	VILGPPASGKTTIAMWLCKHNSLLTLENLINESFSYATARELYLQKTVPSALLVQ	120	
Qy	121	LIOERLAEDCTIKGWLDCGIPETREQALRIOTLIGITPRHVLSAPDTVLIERNLGRI	180	
Db	121	LIOERLAEDCTIKGWLDCGIPETREQALRIOTLIGITPRHVLSAPDTVLIERNLGRI	180	
Qy	181	DPQTEIYHTTFDPPSEIQRNLMPEDISELETAQKLEYHNRNVRVPSYKILKVI	240	
Db	181	DPQTEIYHTTFDPPSEIQRNLMPEDISELETAQKLEYHNRNVRVPSYKILKVI	240	
Qy	241	SADQPCVDVFFQALTYVQSNHRTNAPFTPRVLLGPGVSGSKLQAALLAKYRLVNVCCG	300	
Db	241	SADQPCVDVFFQALTYVQSNHRTNAPFTPRVLLGPGVSGSKLQAALLAKYRLVNVCCG	300	
Qy	301	QLLKEAVADRTTFCGELIQPFKEKMAVPSLIMKVLSDLDQDCIQKGVHLGVPRDL	360	
Db	301	QLLKEAVADRTTFCGELIQPFKEKMAVPSLIMKVLSDLDQDCIQKGVHLGVPRDL	360	

361 QAHLLNRLGYNPNRVPFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
361 QAHLLNRLGYNPNRVPFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
421 NPKDAEQVKLMDLFYRNSADLEQLYGSAITLNGDDPVTVEYIESGLINPLPKIP 479
421 NPKDAEQVKLMDLFYRNSADLEQLYGSAITLNGDDPVTVEYIESGLINPLPKIP 479
RESULT 2
US-10-141-634-4
; Sequence 4, Application US/10141634
; Patent No. 6734010
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6734010el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141.634
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 94
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-141-634-4
Query Match 19.6%; Score 491; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.2e-43; Indels 0; Gaps 0;
Matches 94; Conservative 0; Mismatches 0;
386 MERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQPKDAEQVKLMDLFYRNSADLEQ 445
1 MERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQPKDAEQVKLMDLFYRNSADLEQ 60
446 LYGSAITLNGDDPVTVEYIESGLINPLPKIP 479
61 LYGSAITLNGDDPVTVEYIESGLINPLPKIP 94
RESULT 3
US-09-328-352-5675
; Sequence 5675, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5675
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5675
Query Match 11.2%; Score 280.5; DB 4; Length 222;
Best Local Similarity 29.6%; Pred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 93; Indels 17; Gaps 5;
267 FTRVLLGPGVGSKSLQAALLAQKYLRLNVCCGQLLKEAVADRTTFGLIQPFPEKEWA 326
4 FFWRIILLGPGGAGKTQAQKIVEQFVHAISTGDMRAIRREGTGLKAKSVMSGGL 63
327 VPSLLMKVLSQRLDQDCIQKGMVLHGVRDLQAHLLNR----LGYNPNRVFFLNVPFDSIM 386

64 VSDLLIIGLVKRIQAQDCV--NGCIFDGFRTTPQAALKEKGLSIDHVIIDVPEEIV 122
387 ERLTLRRIDPVTGERYHLMYKPPPTM----EIQARLLQPKDAEQVKLMDLFYRNSAD 442
123 KRLSGRRQHPASGRVYHVYVNPFPKVEGKDDTGTGDLVQRDDQSETIRKSLASH--TE 179
443 LEQLYG--SAITLNGDDP-----YTVFEYIESGLINPLPK 476
180 TEQLVGFYQGAASGENAPTYDKLDGLRTIEDVQKDLFNILDK 222
RESULT 4
US-09-583-110-4124
; Sequence 4124, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4124
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4124
Query Match 10.9%; Score 273; DB 4; Length 212;
Best Local Similarity 31.6%; Pred. No. 5.5e-20;
Matches 67; Conservative 46; Mismatches 85; Indels 14; Gaps 4;
271 VLLGPGVGSKSLQAALLAQKYLRLNVCCGQLLKEAVADRTTFGLIQPFPEKEWAVPS 330
3 LLTMGLPGAGKTQAQKIVEQFVHAISTGDMRAIRREGTGLKAKSVMSGGL 62
331 LLMKVLSQLDQDCIQKGMVLHGVRDLQAHLLNR----LGYNPNRVFFLNVPFDSIM 386
63 VTNGIVKRLSQDDIKETGTLGYPRTIEQAHLDKTLAELGIELEGVINIEVNPDSLL 122
387 ERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQPKDAEQVKLMDLFYRNSADLEQ 446
123 ERLSGRIIHRVTGETFHKVFNPPVDYK-BEDYYQREDDKPTVKRLDV---NIAQGEPI 178
447 Y-----GSAITLNGDDPVTVEYIESGLIN 472
179 IAHYRAKGLVHDIEGNDINDVFSIDIEKVLTN 210
RESULT 5
US-09-107-433-4765
; Sequence 4765, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA


```

FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-08-829-027-5

Query Match          9.6%; Score 240; DB 2; Length 223;
Best Local Similarity 29.6%; Pred. No. 1.6e-16;
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;

QY      270 RVLGLPGVSGKSLQALLAQKRLVNVCCGQLLKEAVADRTTFGLIQPFPEKEMAVPD 329
Db      7 RAVILGPPSGKGTVCQRIAQNFGLQHLSSGHFLRENIKASTVEVGMAKQYIEKSLVDP 66

QY      330 SILMKVLSORLDQDQCIQKG--WVLHGVPRLDQAHLLNRLGYNPNRVPFLNVPDFSIME 387
Db      67 HWITKIMSELEN-----RRGQHWLLDGFPTLQGAELDKI--CEVDLVISLNIPTFLKD 121

QY      388 RLTLRRIDPVTGERYHLMKPPPTWETQ-----ARLQNPDAEQVKLXMDLIFYRNSADL 443
Db      122 RLRSRWIHPSPGRVNLDFNPHVGHGDDVTGTGFLVQGEDDKPEAVARLQYKQVAKPV 181

QY      444 EQLYGSAITL---NGDQD-----PYTVFVIESGIINPLPKK 477
Db      182 IELYKSRGVLIHQFSGTETNKIWPVYILF-----SNKITPIQSK 220

RESULT 10
US-09-225-366-5
; Sequence 5, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,027
; FILING DATE:

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QY      436 ---FYRNSADLEQLYGS 449
      :| | | | :| | |
Db      189 ILEYNNKGVLKNIDGS 205

RESULT 8
US-09-710-279-1580
; Sequence 1580, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1580
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1580

Query Match          9.7%; Score 242.5; DB 4; Length 215;
Best Local Similarity 28.4%; Pred No. 8.3e-17;
Matches 56; Conservative 47; Mismatches 75; Indels 19; Gaps 4;

QY      271 VLLGPGVSGKSLQAAIAQYRLVNVCCGQLLKEAVADRTTFGELIQPFPEKEMAVPDS 330
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3 ILMGLPGAGKGTQASEIVKKFPPIPHISTGDMFRKAIKDETDLGKKAQSYMDRGELVPDE 62

QY      331 LMKVLSQRLDQDQDCIQKGVILHGVPRDLDDQAHLLNRLGYNPNR----VFFLNVPFDSIM 386
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      63 VTVGVIVKGRISDDA-KGFLDGFPRIDQAESLSQIMSELDREIDAVINIEVPEELM 121

QY      387 ERLTLRRIDPVTGGRYHLMYKPPPTWEI-----QALLQNPKDAEQVKLKMDDL----- 435
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      122 NLTGRRICEKCGTTHLVFNPKPDGICDIDGGKLYQREDNPETVGNRLSVNVVKQSKP 181

QY      436 ---FYRNSADLEQLYGS 449
      :| | | | :| | |
Db      182 ILEYNNKGVLKNIDGS 198

RESULT 9
US-08-829-027-5
; Sequence 5, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,027

```

ATTORNEY/AGENT INFORMATION:
NAMS: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-09-225-366-5

Query Match 9.6%; Score 240; DB 3; Length 223;
Best Local Similarity 29.6%; Pred. No. 1.6e-16;
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;

QY 270 RVLLGPGVSGKSLQAALLAOKYRLNVCCGQLLKEAVADRTTFGELIQPFPEKEMAVPD 329
DB 7 RAVILGPGSGKGTVCORIAQNFGHLSSGHFLRENKASTEVGENAKQYIEKSLVDP 66
QY 330 SLLMKVLSQRLLDQDCIQKG--WVLHGVRPRLDQAHLLNRLGYNPNRVFFLNVFDSIME 387
DB 67 HVITKLMSELEN-----RRQHWLLDGFPTLQGAALDKI-CEVDIVISLNIPTFETLKD 121
QY 388 RLTLRRIDPVTGERYHLMYKPPPTMEIQ-----ARLLQNPKDAEBOVKLMDLFYRNSADL 443
DB 122 RLSRRWIHPSPGRVYNLDNPNPHVHGIDVDVTGEPLVQOEDDKPEAVALRLQYKQVAPV 181
QY 444 EOLYGSATL---NGDQD-----PVTVFYIESGIINPLPKK 477
DB 182 IELYKRGVLHQFSGTETNKIWPYVYTLF-----SNKITPQSK 220

RESULT 11

US-09-949-016-9245
Sequence 9245, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 9245
LENGTH: 273
TYPE: PRT
ORGANISM: Human
US-09-949-016-9245

Query Match 9.6%; Score 240; DB 4; Length 273;
Best Local Similarity 29.6%; Pred. No. 2.2e-16;
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;

QY 270 RVLLGPGVSGKSLQAALLAOKYRLNVCCGQLLKEAVADRTTFGELIQPFPEKEMAVPD 329
DB 57 RAVILGPGSGKGTVCORIAQNFGHLSSGHFLRENKASTEVGENAKQYIEKSLVDP 116

QY 330 SLLMKVLSQRLLDQDCIQKG--WVLHGVRPRLDQAHLLNRLGYNPNRVFFLNVFDSIME 387
DB 67 HVITKLMSELEN-----RRQHWLLDGFPTLQGAALDKI-CEVDIVISLNIPTFETLKD 171
QY 388 RLTLRRIDPVTGERYHLMYKPPPTMEIQ-----ARLLQNPKDAEBOVKLMDLFYRNSADL 443
DB 172 RLSRRWIHPSPGRVYNLDNPNPHVHGIDVDVTGEPLVQOEDDKPEAVALRLQYKQVAPV 231
QY 444 EOLYGSATL---NGDQD-----PVTVFYIESGIINPLPKK 477
DB 232 IELYKRGVLHQFSGTETNKIWPYVYTLF-----SNKITPQSK 270

RESULT 12

US-09-489-039A-12712
Sequence 12712, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12712
LENGTH: 225
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12712

Query Match 9.5%; Score 238; DB 4; Length 225;
Best Local Similarity 29.9%; Pred. No. 2.6e-16;
Matches 56; Conservative 46; Mismatches 75; Indels 10; Gaps 4;

QY 57 VPRIVILGPPASGKTTIAMLCKHLNLSLLTLENLI---LNEFSVTATEARRLYLQKTV 113
DB 11 VMRILLGAPGAGKGTQAQFIMEKYGIPQISTGDMRLRAAVKSGSELGKQAKIMDAGKLV 70
QY 114 PSALLVOLIOERLAEEECIKOGWLLDGPETREOALRIQTLGTPRHVIVLSADPTVLIE 173
DB 71 TDELVIALVKERIAHEDC-RNGFLDGFPTIIPQAMKEAGITVDYVLEFDVDELIVD 129
QY 174 RNGLKRIDPQTGEIYHTTFDWPPESEIQN-----RLMVPEIDISELETAOKLLEYHRNIVR 228
DB 130 RIVGRKVAHSGRVYHKFN-PPKVGKDDVTGEBELTTRKDDQEBTVEKRLVYHQMTAP 188
QY 229 VIPSYPK 235
DB 189 LIGYTK 195

RESULT 13

US-09-543-681A-7057
Sequence 7057, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7057
LENGTH: 223
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7057

us-10-798-773-2.ra1

Mon Mar 21 09:11:07 2005

```
Query Match          9.5%; Score 236.5; DB 4; Length 223;
Best Local Similarity 28.7%; Pred. No. 3.7e-16;
Matches 54; Conservative 41; Mismatches 82; Indels 11; Gaps 3;

Qy 267 FTRVLLGPGVSGKSLQAALLAQKYLNVNCGQLLKEAVADRTTFFGELIQPFPEKEMAVPD 326
Db 8 YAMRIILLGPGAGKGTOAQFIKENYGIPIQSTGDMRLRAAVSAGTELGLKAKALMDNGQL 67
Qy 327 VPDLSLLMKVLSQRDLQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPPDSIM 386
Db 68 VTDELVALVKERIKQDC-RNGFLLDGFFRTTIPQADAMKEAGINVDVLEFAVPDEIIV 126
Qy 387 ERLTLRIDPVTGGRYHLMYKPPPTMEIQAR-----LQNPKDAEEQVKLWMDLFYRN 439
Db 127 ERIVGRRVHAPSGRVTYHKFNPP---KVENRDVDTGSELTTTRKDDQDETVRKRLIHYHSQ 183
Qy 440 SADLEQLY 447
Db 184 TAPLVSY 191

RESULT 14
US-08-027-3
; Sequence 3, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,027
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 217576
; US-08-829-027-3

Query Match          9.3%; Score 233.5; DB 2; Length 227;
Best Local Similarity 30.4%; Pred. No. 7.8e-16;
Matches 59; Conservative 37; Mismatches 81; Indels 17; Gaps 4;

Qy 270 RVLLGPGVSGKSLQAALLAQKYLNVNCGQLLKEAVADRTTFFGELIQPFPEKEMAVPD 329
Db 9 RAAIMGAPGSGKGTSSRITKHFELKHLSSGDLRLDNMLRGTEIGVLAKTFIDQKGLIPD 68
Qy 330 SLLMKVLSQRDLQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPPDSIMERL 389
Db 69 DVMTRLVHELH--KNLTQYNWLLDGGFFRTLPQAEALDR-AYQIDTVNLNVPEVIKORL 125
Qy 390 TLRIDPVTGGRYHLMYKPPPTMEIQ-----ARLQNPKDAEEQVKLWMDL----- 435
Db 126 TARMHFGSGRVYNIENFPKPTMGIDDLTGTEPLVQREDDRPETVVKLKAYEAQTEPVL 185
Qy 436 FYRNSADLEQLYS 449
Db 186 YRKKGVLETFSGT 199

RESULT 15
US-09-225-366-3
; Sequence 3, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,027
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 217576
; US-09-225-366-3

Query Match          9.3%; Score 233.5; DB 3; Length 227;
Best Local Similarity 30.4%; Pred. No. 7.8e-16;
Matches 59; Conservative 37; Mismatches 81; Indels 17; Gaps 4;

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Db 9 RAAIMGAPGSGKGTSSRITKHFELKHLSSGDLRLDNMLRGTEIGVLAKTFIDQKGLIPD 68
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Mon Mar 21 09:11:07 2005

us-10-798-773-2.ra1

Page 7

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Qy      390 TLRRIDPVTGERYHLMYKPPPTMEIQ-----ARLLQNPKDABEQVKLKMDL----- 435
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Search completed: March 18, 2005, 15:22:28
Job time : 50 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:20:58 ; Search time 149 Seconds
(without alignments)
1062.612 Million cell updates/sec

Title: US-10-798-773-2
Perfect score: 2500
Sequence: 1 MDATIAPIRIPPENPOYGE...YTVFYESGIINPLPKIP 479
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1401741 seqs, 330541175 residues
Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
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1	2500	100.0	479	14	US-10-141-634-2	Sequence 2, Appli
2	2500	100.0	479	15	US-10-094-749-3020	Sequence 3020, Ap
3	2500	100.0	479	17	US-10-798-773-2	Sequence 2, Appli
4	1429	57.2	275	15	US-10-104-047-3627	Sequence 3627, Ap
5	1429	57.2	275	15	US-10-311-034-25	Sequence 25, Appl
6	1301	52.0	258	14	US-10-165-800-22	Sequence 22, Appl
7	1166	46.6	236	9	US-09-764-868-870	Sequence 870, App
8	553	22.1	113	9	US-09-764-868-868	Sequence 868, App
9	553	22.1	113	9	US-09-764-868-1179	Sequence 1179, Ap
10	491	19.6	94	14	US-10-141-634-4	Sequence 4, Appli
11	491	19.6	94	17	US-10-798-773-4	Sequence 4, Appli
12	378.5	15.1	307	15	US-10-424-599-268668	Sequence 268668,
13	372.5	14.9	290	16	US-10-437-963-120944	Sequence 120944,

14	372	14.9	284	15	US-10-424-599-191515	Sequence 191515,
15	363.5	14.5	303	15	US-10-425-114-47870	Sequence 47870, A
16	363.5	14.5	309	15	US-10-425-114-59931	Sequence 59931, A
17	363.5	14.5	309	15	US-10-425-114-67019	Sequence 67019, A
18	322.5	12.9	310	16	US-10-767-701-43411	Sequence 43411, A
19	293	11.7	801	16	US-10-437-963-172021	Sequence 172021,
20	281	11.2	212	15	US-10-282-122A-72209	Sequence 72209, A
21	278.5	11.1	217	15	US-10-282-122A-44894	Sequence 44894, A
22	273	10.9	212	16	US-10-474-776-612	Sequence 612, App
23	273	10.9	212	17	US-10-472-928-278	Sequence 278, App
24	272	10.9	212	9	US-09-815-242-13219	Sequence 13219, A
25	272	10.9	212	15	US-10-282-122A-73744	Sequence 73744, A
26	271	10.8	220	15	US-10-282-122A-50136	Sequence 50136, A
27	261	10.4	220	15	US-10-425-114-65308	Sequence 65308, A
28	260.5	10.4	220	15	US-10-282-122A-48201	Sequence 48201, A
29	260	10.4	215	15	US-10-282-122A-52019	Sequence 52019, A
30	259	10.4	215	15	US-10-282-122A-74336	Sequence 74336, A
31	259	10.4	241	16	US-10-767-701-43931	Sequence 43931, A
32	257.5	10.3	214	15	US-10-282-122A-77200	Sequence 77200, A
33	256.5	10.3	218	15	US-10-282-122A-51065	Sequence 51065, A
34	255.5	10.2	218	15	US-10-282-122A-63152	Sequence 63152, A
35	253	10.1	271	15	US-10-425-114-58866	Sequence 58866, A
36	253	10.1	271	15	US-10-425-114-58891	Sequence 58891, A
37	252	10.1	216	15	US-10-282-122A-46134	Sequence 46134, A
38	252	10.1	216	15	US-10-282-122A-71311	Sequence 71311, A
39	252	10.1	242	15	US-10-424-599-155349	Sequence 155349, A
40	251	10.0	221	15	US-10-282-122A-53316	Sequence 53316, A
41	249	10.0	260	15	US-10-425-114-61488	Sequence 61488, A
42	248	9.9	218	15	US-10-282-122A-61353	Sequence 61353, A
43	248	9.9	221	15	US-10-282-122A-49618	Sequence 49618, A
44	247	9.9	216	15	US-10-282-122A-52817	Sequence 52817, A
45	247	9.9	227	16	US-10-437-963-172020	Sequence 172020,

ALIGNMENTS

RESULT 1
US-10-141-634-2
; Sequence 2, Application US/10141634
; Publication No. US20030008365A1
; GENERAL INFORMATION:
; APPLICANT: Yu Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Waake, D. Wade
; TITLE OF INVENTION: No. US20030008365A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141.634
; PRIOR FILING DATE: 2002-05-08
; PRIOR FILING DATE: 2002-05-08
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-141-634-2

Query Match 100.0%; Score 2500; DB 14; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 VILGPPASGKTTIAMWLCKHLNSSLTLENLINFESYATARRLYLQKTVPSALLVQ 120
Qy 121 LIQERLAEDDCIKQWILGIPETREQALRIQTGITPRHVIVLSAPDVTLIERNIGRI 180

Db 121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGITPRHVIIVLSAPDVTVLIERNLGKRI 180
Qy 181 DPQGEIYHTTDFWPPSEIQNRIMWVPEDISELETAQKLEHYHRNIVRVIPSPKILKVI 240
Db 181 DPQGEIYHTTDFWPPSEIQNRIMWVPEDISELETAQKLEHYHRNIVRVIPSPKILKVI 240
Qy 241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLIGPVGSGKSQAALLAQKYLNVNCCG 300
Db 241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLIGPVGSGKSQAALLAQKYLNVNCCG 300
Qy 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSILMKVLSORLDQDQCIQKGMVLHGVPDRDL 360
Db 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSILMKVLSORLDQDQCIQKGMVLHGVPDRDL 360
Qy 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
Db 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
Qy 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKKIP 479
Db 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKKIP 479

RESULT 2

US-10-094-749-3020
; Sequence 3020, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISOMO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3020
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-3020

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Db 61 VILGPPASGKTTIAMWLCKHNSLLTLENLIINEFSYATARRLYLQKTVPSALLVQ 120
Qy 121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGITPRHVIIVLSAPDVTVLIERNLGKRI 180
Db 121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGITPRHVIIVLSAPDVTVLIERNLGKRI 180
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Db 181 DPQGEIYHTTDFWPPSEIQNRIMWVPEDISELETAQKLEHYHRNIVRVIPSPKILKVI 240
Qy 241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLIGPVGSGKSQAALLAQKYLNVNCCG 300
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RESULT 3

US-10-798-773-2
; Sequence 2, Application US/10798773
; Publication No. US20050019885A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qionghu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/798,773
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-798-773-2

Query Match 100.0%; Score 2500; DB 17; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 SAAQPCVDVYQALTYVQSNHRTNAPPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCG 300
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Db 421 NPKDAEQVKLQMDLFYRNSADLEQLYGSAILTNGDDPVTTFVIESGIINPLPKIP 479

RESULT 4

US-10-104-047-3627
; Sequence 3627, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3627
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3627

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Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 120
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Db 121 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLNRLGYNPNRVFFLNVPFDS 180
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Db 181 IMERLTLRRIDPVTGERVHLMYKPPPTMEIQARLLQNPDKDAEQVKLQMDLFYRNSADLE 240
QY 445 QLYGSAILTNGDDPVTTFVIESGIINPLPKIP 479
Db 241 QLYGSAILTNGDDPVTTFVIESGIINPLPKIP 275

RESULT 5

US-10-311-034-25
; Sequence 25, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan

APPLICANT: GANDHI, Ameena R.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: YAO, Monique G.
APPLICANT: LU, Dyung Alina M.
APPLICANT: GREENWALD, Sara R.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: KEARNEY, Liam
APPLICANT: BURFORD, Neil
APPLICANT: NGUYEN, Dannel B.
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HE, Ann
APPLICANT: THORNTON, Michael
APPLICANT: HAFALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: LO, Terence P.
APPLICANT: KHAH, Farrah A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Yalda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GREYER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372,
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
; 25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1' 621293CD1
US-10-311-034-25

Query Match 57.2%; Score 1429; DB 15; Length 275;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 MYPEDISELETAQKLLHYHNRVIRVIPSYPKILKVISADQPCVDVYQALTYVQSNHRTN 264
Db 1 MYPEDISELETAQKLLHYHNRVIRVIPSYPKILKVISADQPCVDVYQALTYVQSNHRTN 60
QY 265 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 324
Db 61 APPTPRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 120
QY 325 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLNRLGYNPNRVFFLNVPFDS 384
Db 121 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLNRLGYNPNRVFFLNVPFDS 180
QY 385 IMERLTLRRIDPVTGERVHLMYKPPPTMEIQARLLQNPDKDAEQVKLQMDLFYRNSADLE 444
Db 181 IMERLTLRRIDPVTGERVHLMYKPPPTMEIQARLLQNPDKDAEQVKLQMDLFYRNSADLE 240
QY 445 QLYGSAILTNGDDPVTTFVIESGIINPLPKIP 479
Db 241 QLYGSAILTNGDDPVTTFVIESGIINPLPKIP 275


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RESULT 9
US-09-764-868-1179
; Sequence 1179, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1179
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-1179

Query Match      22.1%; Score 553; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 RVFFLNVPDSIMERLTERRIDPVTGERVHMYKPPPTMEIQARLLQNPDKADEEQVKLM 433
DB 8 RVFFLNVPDSIMERLTERRIDPVTGERVHMYKPPPTMEIQARLLQNPDKADEEQVKLM 67

QY 434 DLFYRNSADLEQLYGSATLNGDQDPYTVFVIESGIINPLPKIP 479
DB 68 DLFYRNSADLEQLYGSATLNGDQDPYTVFVIESGIINPLPKIP 113

RESULT 10
US-10-141-634-4
; Sequence 4, Application US/10141634
; Publication No. US20030008365A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-634-4

Query Match      19.6%; Score 491; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 MERLTURRIDPVTGERVHMYKPPPTMEIQARLLQNPDKADEEQVKLM 445
DB 1 MERLTURRIDPVTGERVHMYKPPPTMEIQARLLQNPDKADEEQVKLM 60

QY 446 LYGSATLNGDQDPYTVFVIESGIINPLPKIP 479
DB 61 LYGSATLNGDQDPYTVFVIESGIINPLPKIP 94

RESULT 11
US-10-798-773-4
; Sequence 4, Application US/10798773
; Publication No. US20050019885A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/798,773
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-798-773-4

Query Match      19.6%; Score 491; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 MERLTURRIDPVTGERVHMYKPPPTMEIQARLLQNPDKADEEQVKLM 445
DB 1 MERLTURRIDPVTGERVHMYKPPPTMEIQARLLQNPDKADEEQVKLM 60

QY 446 LYGSATLNGDQDPYTVFVIESGIINPLPKIP 479
DB 61 LYGSATLNGDQDPYTVFVIESGIINPLPKIP 94

RESULT 12
US-10-424-599-268668
; Sequence 268668, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 268668
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8462C.1.pap
US-10-424-599-268668

Query Match      15.1%; Score 378.5; DB 15; Length 307;
Best Local Similarity 35.1%; Pred. No. 2.7e-26;
Matches 88; Conservative 45; Mismatches 89; Indels 29; Gaps 5;

QY 220 LEYHVRVIVPSYPKILKVISADQPCVDVFYQALTYVQSNHRTNAPPTPRVLLGLPGVS 279
DB 57 LRYHVT---LPSPTKLV-----NCSTSEPL--KVMISGAPAS 90

QY 280 GKSLQALLAQYRLVNVCCQLLKAVADRTTFBELQPFPEKEMAVPDSLMKVLVSOR 339
DB 91 GKGTQCELVQKFLGVHISTGDLRLRAEVAAGTEIGNKAKEFMNTGQLVDPDEIVTAMVAAR 150

QY 340 LDQDCIQKQWVLHGVPRDLQARHLNRLGYNPNVFFLNVPFDSIMERLTERRIDPVTG 399
DB 151 LAREDEVHRHKGWLLDGYPRSFQAGSLEKMQIRPDVYVILVDVPEILIDRCVGRRLDPVTG 210
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us-10-798-773-2.rapb

Mon Mar 21 09:11:07 2005

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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191515
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14959C.1.pep
; US-10-424-599-191515

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Query Match 14.9%; Score 372.5; DB 16; Length 290;
Best Local Similarity 34.3%; Pred. No. 9e-26; Indels 25; Gaps 3;
Matches 86; Conservative 41; Mismatches 99;
;
QY 228 RVIPSPKILKVSADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGPGVSGKSLQAL 287
DB 57 RSLPRAKVAVKAD-----PL--KVMAGAPASGKGTQCEL 92
QY 288 LAQKRLVNVCCGQLLKEAVADRTTGGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQ 347
DB 93 IKSKYGLVHISAGDLLRAETIAAGSENGKRAKEFMKQGLVPDEIVVMVKERLLQPDQAE 152
QY 348 KGVVLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERHLMYK 407
DB 153 KGWLLDGVPRYSQMALETINRPDIFILLDVPDELLVERVVGRLDPTGKIYHLKYS 212
QY 408 PPPTMEIOARLQNPKEAEQVKLMDFYRNSADLEQLYGSALT-LNGDQDPYTVFEYI 466
DB 213 PPENEIASRLTORFDDTEERKVLRLQTHQNVESLSIYEDVIVEKGDALVDDVFAEI 272
QY 467 ESGIINPLPKK 477
DB 273 DKQLTSSLDKK 283

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RESULT 13
US-10-437-963-120944
; Sequence 120944, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION: Thomas J.
; APPLICANT: La Rosa, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120944
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_24016C.1.pep
; US-10-437-963-120944

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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191515
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14959C.1.pep
; US-10-424-599-191515

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Query Match 14.9%; Score 372; DB 15; Length 284;
Best Local Similarity 34.5%; Pred. No. 9.8e-26; Indels 16; Gaps 2;
Matches 79; Conservative 45; Mismatches 89;
;
QY 265 APPTP-----RVLLGPGVSGKSLQALLAQKRYLVNVCCGQLLKEAVAD 309
DB 47 SPFAPNAIHSFSLSVTNEALNVWISGAPASGKTQCHLITNKYGLVHIAAGDLLRAEIAI 106
QY 310 RTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVVLGVPRDLQAHLLNRLG 369
DB 107 GSDNGKRAKQYMEKQGLVPDEIVVMVKERLLKPDSENGWLLDGPRLSQATALEALG 166
QY 370 YPNRVPFLNVPFDSIMERLTLRRIDPVTGERHLMYKPPPTMEIOARLQNPKEAEQV 429
DB 167 FRPHIFLLLEVEDLVVERVVGRLDPTGKIYHLKYSPPETQBIARLTQREDDTEEKV 226
QY 430 KLMDFLYRNSADLEQLYGS-AITLNGDQDPYTVFEYIESGIINPLPKK 477
DB 227 KLRNLTHQNVESVLSMYKDTIVKINGNVSKBEVFAQIDSAITSLIEER 275

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RESULT 15
US-10-425-114-47870
; Sequence 47870, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47870
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-027-G7_FLI.pep
; US-10-425-114-47870

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Query Match 14.5%; Score 363.5; DB 15; Length 303;
Best Local Similarity 37.3%; Pred. No. 6.6e-25; Indels 1; Gaps 1;
Matches 78; Conservative 40; Mismatches 90;
;
QY 270 RVLLGPGVSGKSLQALLAQKRYLVNVCCGQLLKEAVADRTTGGELIQPFPEKEMAVPD 329
DB 88 KVMISGAPASGKTQCELITKYQLAHISAGDLLRAEIAAGSENGKRAKEFMKQGLVPD 147
QY 330 SLLMKVLSQRLDQDCIQKGVVLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389
DB 148 EIVVMVKERLRQPDQAQENGWLLDGPRLSQATALEALG 207
QY 390 TURRIDPVTGERHLMYKPPPTMEIOARLQNPKEAEQVKLMDFYRNSADLEQLYGS 449
DB 208 VGRRLDPTGKIYHLKYSPPENEIASRLTORFDDTEERKVLRLQTHQNVESLSIYEDVIVEKGDALVDDVFAEI 267

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Mon Mar 21 09:11:07 2005

us-10-798-773-2.rapb

Page 7

QY 450 AIT-LNGQDPYTVFEYIESGIINPLPKK 477
Db 268 IIVKQDATVDVFAKIDELIGSILEKK 296

Search completed: March 18, 2005, 15:33:59
Job time : 153 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 22:35:46 ; Search time 808 Seconds
(without alignments)
10609.705 Million cell updates/sec

Title: US-10-798-773-1
Perfect score: 1440
Sequence: 1 atggacgccactatcgcccc.....tgcacagaaatccccctga 1440

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:**
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
2: /cgn2_6/ptodata/2/pubpna/US07_PCT_NEW_PUB.seq**
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq**
4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
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9: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
10: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
11: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
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21: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
22: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1440	100.0	1440	14	US-10-141-634-1
2	1440	100.0	1440	19	US-10-798-773-1
3	1440	100.0	1579	17	US-10-094-749-1381
4	1440	100.0	1581	18	US-10-478-146-17
5	1170	81.2	1619	17	US-10-104-047-1657
6	1032.8	71.7	1452	14	US-10-165-800-21
7	1027.6	71.4	1223	9	US-09-764-868-257
8	868	60.3	995	17	US-10-311-034-51
9	761	52.8	1778	13	US-10-098-841-257
10	759.8	52.8	774	14	US-10-165-800-23
11	407	28.3	407	10	US-09-918-995-16667

12	366.6	25.5	447	10	US-09-918-995-29164	Sequence 29164, A
13	322	22.4	509	9	US-09-764-868-255	Sequence 255, App
14	322	22.4	510	9	US-09-764-868-566	Sequence 566, App
15	285	19.8	285	14	US-10-141-634-3	Sequence 3, Appli
16	285	19.8	285	19	US-10-798-773-3	Sequence 3, Appli
17	134.6	9.3	545	16	US-10-029-386-5683	Sequence 5683, Ap
18	132	9.2	132	16	US-10-029-386-19439	Sequence 19439, A
19	92.8	6.4	1496	18	US-10-437-963-18461	Sequence 18461, A
20	88	6.1	23865	18	US-10-719-993-7056	Sequence 7056, Ap
21	87	6.0	1165	18	US-10-435-115-16589	Sequence 16589, A
22	87	6.0	1304	17	US-10-435-115-15576	Sequence 15576, A
23	87	6.0	1489	18	US-10-435-115-16966	Sequence 16966, A
24	85.4	5.9	2547	18	US-10-767-701-15490	Sequence 15490, A
25	85.4	5.9	1246	17	US-10-425-114-28385	Sequence 28385, A
26	85.4	5.9	1402	17	US-10-425-114-24964	Sequence 24964, A
27	84	5.7	1894	17	US-10-425-115-169643	Sequence 169643, A
28	81.4	5.7	1410	17	US-10-104-047-1583	Sequence 1583, Ap
29	77.6	5.4	654	17	US-10-424-599-48673	Sequence 48673, A
30	75.8	5.3	1031	17	US-10-282-122A-14881	Sequence 14881, A
31	75.8	5.3	663	17	US-10-424-599-125826	Sequence 125826, A
32	74.4	5.2	1022	18	US-10-282-122A-13434	Sequence 13434, A
33	72.6	5.0	813	13	US-10-767-701-11847	Sequence 11847, A
34	71.6	5.0	1028	18	US-10-027-632-10112	Sequence 10112, A
35	71.6	5.0	813	17	US-10-027-632-10112	Sequence 10112, A
36	71.6	5.0	1028	18	US-10-425-115-145038	Sequence 145038, A
37	69.6	4.8	660	17	US-10-282-122A-12017	Sequence 12017, A
38	69	4.8	642	17	US-10-282-122A-20034	Sequence 20034, A
39	68	4.7	648	9	US-09-815-242-7844	Sequence 7844, Ap
40	68	4.7	648	17	US-10-282-122A-30345	Sequence 30345, A
41	66.4	4.6	645	9	US-09-815-242-7536	Sequence 7536, Ap
42	66.4	4.6	645	17	US-10-282-122A-13952	Sequence 13952, A
43	63.2	4.4	642	17	US-10-282-122A-23787	Sequence 23787, A
44	63.2	4.4	645	9	US-09-815-242-5978	Sequence 5978, Ap
45	63.2	4.4	645	17	US-10-282-122A-6793	Sequence 6793, Ap

ALIGNMENTS

RESULT 1
US-10-141-634-1
; Sequence 1: Application US/10141634
; Publication No. US20030008365A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qionghu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20030008365A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-634-1

Query Match	100.0%	Score 1440;	DB 14;	Length 1440;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGAGCGCCTATCGCCCGCACCTATCGCCCGCGAGATCGCCCGAGTGGGGAGAG	60	
Db	1	ATGGAGCGCCTATCGCCCGCACCTATCGCCCGCGAGATCGCCCGAGTGGGGAGAG	60	
Qy	61	ACCCATCTTCGAGTTGATGAGAAATGCTGGAGCAATCTCTGATCCACGAGCCGAA	120	
Db	61	AACCATCTTCGAGTTGATGAGAAATGCTGGAGCAATCTCTGATCCACGAGCCGAA	120	

QY	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGAGCAACACAAATGTGCCAGGATT	180	QY	1201	AGGTACCACTCATGTATACAGCCACCTCCACCATGGAGATCCAGGCTCGCTCTCTGCAG	1260
DB	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGAGCAACACAAATGTGCCAGGATT	180	DB	1201	AGGTACCACTCATGTATACAGCCACCTCCACCATGGAGATCCAGGCTCGCTCTCTGCAG	1260
QY	181	GTAATATATAGTCTCACCGCTCAGGGAAACAAACAAATAGCAATGTGGCTCTGCAAAAT	240	QY	1261	AACCAAGAGATGTGAAGAGCAGGTCAAGCTGAAATGCACTGTGTCTACAGAACTCA	1320
DB	181	GTAATATATAGTCTCACCGCTCAGGGAAACAAACAAATAGCAATGTGGCTCTGCAAAAT	240	DB	1261	AACCAAGAGATGTGAAGAGCAGGTCAAGCTGAAATGCACTGTGTCTACAGAACTCA	1320
QY	241	CTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTAATAGATTTCTTATACGGCC	300	QY	1321	GCTGACTTGGAGCAGTGTATGGTGGCCATCACTTCAATGGGACCGGACCCATAC	1380
DB	241	CTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTAATAGATTTCTTATACGGCC	300	DB	1321	GCTGACTTGGAGCAGTGTATGGTGGCCATCACTTCAATGGGACCGGACCCATAC	1380
QY	301	ACCAAGCCAGAGGCTTTATCTCAAGGAAGACAGTCTCCAGCGCGCTGCTGCTCCAG	360	QY	1381	ACAGTCTTCGAATCATCGAGGTGGGATCAATTAATCCCTGCCCCAAGAAATCCCTCTGA	1440
DB	301	ACCAAGCCAGAGGCTTTATCTCAAGGAAGACAGTCTCCAGCGCGCTGCTGCTCCAG	360	DB	1381	ACAGTCTTCGAATCATCGAGGTGGGATCAATTAATCCCTGCCCCAAGAAATCCCTCTGA	1440
QY	361	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	420	QY	1440	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	1500
DB	361	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	420	DB	1440	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	1500
QY	421	ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGAC	480	QY	1500	ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGAC	1560
DB	421	ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGAC	480	DB	1500	ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGAC	1560
QY	481	GTCATTGCTGAGTGTCTCCAGACACGCTCTGATCGAGAGAACTTTGGGAAAGAAATC	540	QY	1560	GTCATTGCTGAGTGTCTCCAGACACGCTCTGATCGAGAGAACTTTGGGAAAGAAATC	1620
DB	481	GTCATTGCTGAGTGTCTCCAGACACGCTCTGATCGAGAGAACTTTGGGAAAGAAATC	540	DB	1560	GTCATTGCTGAGTGTCTCCAGACACGCTCTGATCGAGAGAACTTTGGGAAAGAAATC	1620
QY	541	GACCTCTAACTGGAGAGATTATACACACCTTTGATCTGGCCACCGGATCTGAATC	600	QY	1620	GACCTCTAACTGGAGAGATTATACACACCTTTGATCTGGCCACCGGATCTGAATC	1680
DB	541	GACCTCTAACTGGAGAGATTATACACACCTTTGATCTGGCCACCGGATCTGAATC	600	DB	1620	GACCTCTAACTGGAGAGATTATACACACCTTTGATCTGGCCACCGGATCTGAATC	1680
QY	601	CAGACCGCTCTCATGCTGCGAGGACATCTCAGAGCTGGAGAGCGCTCAGAAACTGCTG	660	QY	1680	CAGACCGCTCTCATGCTGCGAGGACATCTCAGAGCTGGAGAGCGCTCAGAAACTGCTG	1740
DB	601	CAGACCGCTCTCATGCTGCGAGGACATCTCAGAGCTGGAGAGCGCTCAGAAACTGCTG	660	DB	1680	CAGACCGCTCTCATGCTGCGAGGACATCTCAGAGCTGGAGAGCGCTCAGAAACTGCTG	1740
QY	661	GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTACCCCAAAATCTCAAAATCATC	720	QY	1740	GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTACCCCAAAATCTCAAAATCATC	1800
DB	661	GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTACCCCAAAATCTCAAAATCATC	720	DB	1740	GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTACCCCAAAATCTCAAAATCATC	1800
QY	721	AGTGTGACAGCAGTGTGAGACCTCTTACAGGCTCTGACCTATGTCCAAAGCAAC	780	QY	1800	AGTGTGACAGCAGTGTGAGACCTCTTACAGGCTCTGACCTATGTCCAAAGCAAC	1860
DB	721	AGTGTGACAGCAGTGTGAGACCTCTTACAGGCTCTGACCTATGTCCAAAGCAAC	780	DB	1800	AGTGTGACAGCAGTGTGAGACCTCTTACAGGCTCTGACCTATGTCCAAAGCAAC	1860
QY	781	CATCGTACTAATGCCCGCTTCAACCCGAGGGTGTCTGCTCGGCGCTGTGGCAGTGGG	840	QY	1860	CATCGTACTAATGCCCGCTTCAACCCGAGGGTGTCTGCTCGGCGCTGTGGCAGTGGG	1920
DB	781	CATCGTACTAATGCCCGCTTCAACCCGAGGGTGTCTGCTCGGCGCTGTGGCAGTGGG	840	DB	1860	CATCGTACTAATGCCCGCTTCAACCCGAGGGTGTCTGCTCGGCGCTGTGGCAGTGGG	1920
QY	841	AAAAGTCTGACGCGCCCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTGTGGG	900	QY	1920	AAAAGTCTGACGCGCCCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTGTGGG	1980
DB	841	AAAAGTCTGACGCGCCCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTGTGGG	900	DB	1920	AAAAGTCTGACGCGCCCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTGTGGG	1980
QY	901	CAATCTGTGAAGAGCTGTGGCAGATAGACACAGCTTTGGCGAGCTCATCCAGCCCTTC	960	QY	1980	CAATCTGTGAAGAGCTGTGGCAGATAGACACAGCTTTGGCGAGCTCATCCAGCCCTTC	2040
DB	901	CAATCTGTGAAGAGCTGTGGCAGATAGACACAGCTTTGGCGAGCTCATCCAGCCCTTC	960	DB	1980	CAATCTGTGAAGAGCTGTGGCAGATAGACACAGCTTTGGCGAGCTCATCCAGCCCTTC	2040
QY	961	TTTGAAGAGAGATGGCAGTCTCTGACGCTCTCTCATGAAGGCTGTGAGCCAGCGCTG	1020	QY	2040	TTTGAAGAGAGATGGCAGTCTCTGACGCTCTCTCATGAAGGCTGTGAGCCAGCGCTG	2100
DB	961	TTTGAAGAGAGATGGCAGTCTCTGACGCTCTCTCATGAAGGCTGTGAGCCAGCGCTG	1020	DB	2040	TTTGAAGAGAGATGGCAGTCTCTGACGCTCTCTCATGAAGGCTGTGAGCCAGCGCTG	2100
QY	1021	GACAGCAGAGCTGTGATCAGAAAGGCTGGTGTCTACAGGCTCCCGGGGACCTCCGAC	1080	QY	2100	GACAGCAGAGCTGTGATCAGAAAGGCTGGTGTCTACAGGCTCCCGGGGACCTCCGAC	2160
DB	1021	GACAGCAGAGCTGTGATCAGAAAGGCTGGTGTCTACAGGCTCCCGGGGACCTCCGAC	1080	DB	2100	GACAGCAGAGCTGTGATCAGAAAGGCTGGTGTCTACAGGCTCCCGGGGACCTCCGAC	2160
QY	1081	CAGSCACCTGTGAAACCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGG	1140	QY	2160	CAGSCACCTGTGAAACCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGG	2220
DB	1081	CAGSCACCTGTGAAACCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGG	1140	DB	2160	CAGSCACCTGTGAAACCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGG	2220
QY	1141	CAATTCATTCATATGAGCGGCTGACTCTGAGAGAGATTCAGTCCAGTCACTGGGAA	1200	QY	2220	CAATTCATTCATATGAGCGGCTGACTCTGAGAGAGATTCAGTCCAGTCACTGGGAA	2280
DB	1141	CAATTCATTCATATGAGCGGCTGACTCTGAGAGAGATTCAGTCCAGTCACTGGGAA	1200	DB	2220	CAATTCATTCATATGAGCGGCTGACTCTGAGAGAGATTCAGTCCAGTCACTGGGAA	2280

RESULT 2

US-10-798-773-1
; Sequence 1, Application US/10798773
; Publication NO. US20050019885A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qionghu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/798,773
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-773-1

Query Match 100.0%; Score 1440; DB 19; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGCGCACATATCGCCCGCACCGTATCCCGCGAGATGCCCGAGTACCGGAGGAG	60	QY	1	ATGAGCGCACATATCGCCCGCACCGTATCCCGCGAGTACCGGAGGAG	60
DB	1	ATGAGCGCACATATCGCCCGCACCGTATCCCGCGAGTACCGGAGGAG	60	DB	1	ATGAGCGCACATATCGCCCGCACCGTATCCCGCGAGTACCGGAGGAG	60
QY	61	AACCAATCTTCGAGTTGATGACAGAAATCTCTGATGATCCAGCCCGAA	120	QY	61	AACCAATCTTCGAGTTGATGACAGAAATCTCTGATGATCCAGCCCGAA	120
DB	61	AACCAATCTTCGAGTTGATGACAGAAATCTCTGATGATCCAGCCCGAA	120	DB	61	AACCAATCTTCGAGTTGATGACAGAAATCTCTGATGATCCAGCCCGAA	120
QY	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAACACAAATGTGCCAGATT	180	QY	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAACACAAATGTGCCAGATT	180
DB	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAACACAAATGTGCCAGATT	180	DB	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAACACAAATGTGCCAGATT	180
QY	181	GTAATATATAGTCCACCGCTCAGGGAAACAAACAAATAGCAATGTGGCTCTGCAAAAT	240	QY	181	GTAATATATAGTCCACCGCTCAGGGAAACAAACAAATAGCAATGTGGCTCTGCAAAAT	240
DB	181	GTAATATATAGTCCACCGCTCAGGGAAACAAACAAATAGCAATGTGGCTCTGCAAAAT	240	DB	181	GTAATATATAGTCCACCGCTCAGGGAAACAAACAAATAGCAATGTGGCTCTGCAAAAT	240
QY	241	CTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTAATAGATTTCTTATACGGCC	300	QY	241	CTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTAATAGATTTCTTATACGGCC	300
DB	241	CTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTAATAGATTTCTTATACGGCC	300	DB	241	CTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTAATAGATTTCTTATACGGCC	300
QY	301	ACCAAGCCAGAGGCTTTATCTCAAGGAAGACAGTCTCCAGCGCGCTGCTGCTCCAG	360	QY	301	ACCAAGCCAGAGGCTTTATCTCAAGGAAGACAGTCTCCAGCGCGCTGCTGCTCCAG	360
DB	301	ACCAAGCCAGAGGCTTTATCTCAAGGAAGACAGTCTCCAGCGCGCTGCTGCTCCAG	360	DB	301	ACCAAGCCAGAGGCTTTATCTCAAGGAAGACAGTCTCCAGCGCGCTGCTGCTCCAG	360
QY	361	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	420	QY	361	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	420
DB	361	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	420	DB	361	CTGATTCAGGAACGCTGGCTGGAAGAGATTCGATCAAGAGGCTGGATTCGGATGGC	420

QY	421	ATCCCTGAGACGCGTGTGACGAGCTCTGAGGATCCAGACCTCTGGGGATCACACCCAGACAC	480
DB	421	ATCCCTGAGACGCGTGTGACGAGCTCTGAGGATCCAGACCTCTGGGGATCACACCCAGACAC	480
QY	481	GTCAATTGTGCTGAGTGTCTCCAGACAGCGTCTCTGATCGAGAGAAACTTTGGGGAGAGAAATC	540
DB	481	GTCAATTGTGCTGAGTGTCTCCAGACAGCGTCTCTGATCGAGAGAAACTTTGGGGAGAGAAATC	540
QY	541	GACCCCTCAAACTGGAGAGATTATCACACCACTTTGACCTGGCCACCGGAATCTGAAATC	600
DB	541	GACCCCTCAAACTGGAGAGATTATCACACCACTTTGACCTGGCCACCGGAATCTGAAATC	600
QY	601	CAGAACCGGTCTCATGCTGGCCAGAGGACATCTCAGAGCTTGAGACGGCTCAGAAACTGCTG	660
DB	601	CAGAACCGGTCTCATGCTGGCCAGAGGACATCTCAGAGCTTGAGACGGCTCAGAAACTGCTG	660
QY	661	GAGTATCATPAGAGACATGTCAGGGTCAATCCCTCTTACCCCAAATCCTCAAAGTCATC	720
DB	661	GAGTATCATPAGAGACATGTCAGGGTCAATCCCTCTTACCCCAAATCCTCAAAGTCATC	720
QY	721	AGTGTCTGACAGCCATGTGTGGACGTCTTCTACGAGCTCTGACTATGTGCCAAAGCAAC	780
DB	721	AGTGTCTGACAGCCATGTGTGGACGTCTTCTACGAGCTCTGACTATGTGCCAAAGCAAC	780
QY	781	CATCGTACTAATGCCCGTTTCACCCAGAGGTGTGTCTCGGGCCCTGTGGGCGAGTGGG	840
DB	781	CATCGTACTAATGCCCGTTTCACCCAGAGGTGTGTCTCGGGCCCTGTGGGCGAGTGGG	840
QY	841	AAAAGTCTGCAGGCGCGCTCTCGGCCAGAGAAATACAGGCTTGTCTGCTGTGGG	900
DB	841	AAAAGTCTGCAGGCGCGCTCTCGGCCAGAGAAATACAGGCTTGTCTGCTGTGGG	900
QY	901	CAACTCTGAAAGAGGCTGTGGAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC	960
DB	901	CAACTCTGAAAGAGGCTGTGGAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC	960
QY	961	TTTGGAAAAGGAGATGGCAGTTCCTCAGACGCTCTCTCATGAAGGTGTGAGCCAGAGCCGCTG	1020
DB	961	TTTGGAAAAGGAGATGGCAGTTCCTCAGACGCTCTCTCATGAAGGTGTGAGCCAGAGCCGCTG	1020
QY	1021	GACCAGCAGGACTGCATCCAGAAAGGCTGGGTGCTACACGGGCTCCGCGGGACCTGCAC	1080
DB	1021	GACCAGCAGGACTGCATCCAGAAAGGCTGGGTGCTACACGGGCTCCGCGGGACCTGCAC	1080
QY	1081	CAGGCACACCTGCTGAAACCGCTGGGCTCAAAATCCACAGGGTGTTCCTGTAATGTG	1140
DB	1081	CAGGCACACCTGCTGAAACCGCTGGGCTCAAAATCCACAGGGTGTTCCTGTAATGTG	1140
QY	1141	CCATTTGANTTCATCATGAGAGGCGTGACTCTGAGAGAAATTTGATCCAGTCACTGGGGAA	1200
DB	1141	CCATTTGANTTCATCATGAGAGGCGTGACTCTGAGAGAAATTTGATCCAGTCACTGGGGAA	1200
QY	1201	AGGTACCACTCATGTPACAACCACTCCCAACCATGGAGATCCAGGCTGGCTCTCTGCGAG	1260
DB	1201	AGGTACCACTCATGTPACAACCACTCCCAACCATGGAGATCCAGGCTGGCTCTCTGCGAG	1260
QY	1261	AACCCAAAGGATGTGAAGACAGGTCAGAGCTGAAATATGGACCTGTTCTACAGGAACTCA	1320
DB	1261	AACCCAAAGGATGTGAAGACAGGTCAGAGCTGAAATATGGACCTGTTCTACAGGAACTCA	1320
QY	1321	GCTGACTTGGAGCAGTGTGATGGTGGGCCATCACCTCAATGGGACACGAGACCAATAC	1380
DB	1321	GCTGACTTGGAGCAGTGTGATGGTGGGCCATCACCTCAATGGGACACGAGACCAATAC	1380
QY	1381	ACAGTCTTCGAATACATCGAGATGGGATTAATATCCCTGCGCCCAAGAAATCCCTCTGA	1440
DB	1381	ACAGTCTTCGAATACATCGAGATGGGATTAATATCCCTGCGCCCAAGAAATCCCTCTGA	1440

; Publication No. US20030219741A1
 ; GENERAL INFORMATION
 ; APPLICANT: ISOGA, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: TSUKU, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKI, ICHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTUYUKI
 ; APPLICANT: KAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1381
 ; LENGTH: 1579
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-094-749-1381

Query Match	100.0%;	Score 1440;	DB 17;	Length 1579;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 1440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGCCCACTATCGCCCGCAGCCGATATCCCCCGAGATGCCAGTACGGGAGGAG	60	
DB	30	ATGGAGCCCACTATCGCCCGCAGCCGATATCCCCCGAGATGCCAGTACGGGAGGAG	89	
QY	61	AACCACATCTTCAGATTGATSCAGAAATCTGGGCAATCTCGATCCACAGCCCGAA	120	
DB	90	AACCACATCTTCAGATTGATSCAGAAATCTGGGCAATCTCGATCCACAGCCCGAA	149	
QY	121	GATCCCATCCCTTCATGATCCAGACCTTCGATAGAGACAGCAATGTGCCAGGATT	180	
DB	150	GATCCCATCCCTTCATGATCCAGACCTTCGATAGAGACAGCAATGTGCCAGGATT	209	
QY	181	GTAATATTAGGTCACCCGCTCAGGAAAAACAATAGCAATGTGGCTCTGCAAAACAT	240	
DB	210	GTAATATTAGGTCACCCGCTCAGGAAAAACAATAGCAATGTGGCTCTGCAAAACAT	269	
QY	241	CTGAACACGAGTCTCTCAACCTCGGAGAACCTGATCTTAAATAGTTTTCTATACGCC	300	
DB	270	CTGAACACGAGTCTCTCAACCTCGGAGAACCTGATCTTAAATAGTTTTCTATACGCC	329	
QY	301	ACCGAAGCCAGAAAGCTTTATCTGCAAAAGGAGACAGTTCCACAGCGCGTCTGCTCCAG	360	
DB	330	ACCGAAGCCAGAAAGCTTTATCTGCAAAAGGAGACAGTTCCACAGCGCGTCTGCTCCAG	389	
QY	361	CTGATTTCAGGAACCCCTGGCTGAAGAGGATTCGATCAGCAGGGCTGGATTCTGGATGGC	420	
DB	390	CTGATTTCAGGAACCCCTGGCTGAAGAGGATTCGATCAGCAGGGCTGGATTCTGGATGGC	449	
QY	421	ATCCCTCTGAGACCGCTGAGCAGGCTCTGAGGATTCAGACCCCTGGGGATCAACCCAGACAC	480	
DB	450	ATCCCTCTGAGACCGCTGAGCAGGCTCTGAGGATTCAGACCCCTGGGGATCAACCCAGACAC	509	
QY	481	GTCAATTGTCAGTGTCTCAGACACCGTCTCGATCTCGAGAGAAACTTTGGGAAAGAAATC	540	

Db 510 GTCAATGCTGAGTCTCCAGACACGGTCTGATCGAGAGAACTTGGGAGAGAAATC 569
Qy 541 GACCTCAAACTGAGAGATTATCACACCACTTTGACTGGCCACCCGAAATCTGAAATC 600
Db 570 GACCTCAAACTGAGAGATTATCACACCACTTTGACTGGCCACCCGAAATCTGAAATC 629
Qy 601 CAGAACCGTCTCATGCTGCGAGAGGACATCTCAGAGCTGAGAGCGCTCAGAACTGCTG 660
Db 630 CAGAACCGTCTCATGCTGCGAGAGGACATCTCAGAGCTGAGAGCGCTCAGAACTGCTG 689
Qy 661 GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTCTACCCCAAAATCTCAAAGTCATC 720
Db 690 GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTCTACCCCAAAATCTCAAAGTCATC 749
Qy 721 AGTGTGACACGAGCATGCTGAGAGCTCTTCTACAGGCTCTGACCTATGTCCTCAAGCAAC 780
Db 750 AGTGTGACACGAGCATGCTGAGAGCTCTTCTACAGGCTCTGACCTATGTCCTCAAGCAAC 809
Qy 781 CATGTAATAATGCCCGCTTCAACCCGAGGCTGCTGCTCGGGCTGTGGCAGTGGG 840
Db 810 CATGTAATAATGCCCGCTTCAACCCGAGGCTGCTGCTCGGGCTGTGGCAGTGGG 869
Qy 841 AAAAGTCTGAGGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGCTGCTGTGGG 900
Db 870 AAAAGTCTGAGGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGCTGCTGTGGG 929
Qy 901 CAACTGCTGAAAGAGGCTGTGCGAGATAGACACGCTTGGCGAGCTCATCCAGCCCTC 960
Db 930 CAACTGCTGAAAGAGGCTGTGCGAGATAGACACGCTTGGCGAGCTCATCCAGCCCTC 989
Qy 961 TTTGAAAGGAGATGGCAGTCTTCTCAGAGCTCTCTCATGAGGCTGCTGAGCCAGGCTG 1020
Db 990 TTTGAAAGGAGATGGCAGTCTTCTCAGAGCTCTCTCATGAGGCTGCTGAGCCAGGCTG 1049
Qy 1021 GACACGAGGATGCTATCCAGAAAGGCTGGGTGTCTACACGGCTCCCGCGGAGCTCGAC 1080
Db 1050 GACACGAGGATGCTATCCAGAAAGGCTGGGTGTCTACACGGCTCCCGCGGAGCTCGAC 1109
Qy 1081 CAGGCAACCTGCTGACCGCTGGGTGTCTATCCCAAGGCTGTTTCTCAATGTG 1140
Db 1110 CAGGCAACCTGCTGACCGCTGGGTGTCTATCCCAAGGCTGTTTCTCAATGTG 1169
Qy 1141 CCAATTTGATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
Db 1170 CCAATTTGATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1229
Qy 1201 AGGTACACCTCATGTACAGCCACTCCACATGAGATCCAGGCTCGCTCTCTGAG 1260
Db 1230 AGGTACACCTCATGTACAGCCACTCCACATGAGATCCAGGCTCGCTCTCTGAG 1289
Qy 1261 AACCAAGGATGCTGAAGAGAGGCTCAAGCTGAAATGAGCTGTTTCTACAGGAATCA 1320
Db 1290 AACCAAGGATGCTGAAGAGAGGCTCAAGCTGAAATGAGCTGTTTCTACAGGAATCA 1349
Qy 1321 GCTGACTTGGAGAGTTGATAGGCTGGCCATCACCTCAATGGGGACAGACCCATAC 1380
Db 1350 GCTGACTTGGAGAGTTGATAGGCTGGCCATCACCTCAATGGGGACAGACCCATAC 1409
Qy 1381 ACAGTCTCGAATACATCGAGTGGGATCATTAATCCCTGCGCCAGAAATATCCCTGGA 1440
Db 1410 ACAGTCTCGAATACATCGAGTGGGATCATTAATCCCTGCGCCAGAAATATCCCTGGA 1469

RESULT 4
US-10-478-146-17
; Sequence 17, Application US/10478146
; Publication No. US20040203097A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; YUE, Henry;
; APPLICANT: LU, Dying Aina M.; AZIMZAI, Yalda;
; APPLICANT: DING, Li; LEE, Ernestine A.;
; APPLICANT: HAFALIA, April J.A.; BECHA, Shanya D.;

; APPLICANT: TANG, Y. Tom; LAL, Preeti G.;
; APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
; APPLICANT: RAMKUMAR, Javalakxmi; ELLIOTT, Vicki S.;
; APPLICANT: ARVIZU, Chandra S.; LUO, Wen;
; APPLICANT: SWARNAKAR, Anita; DUGGAN, Brendan M.;
; APPLICANT: TRAN, Uyen K.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; YAO, Monique G.;
; APPLICANT: KHAN, Farrah A.; BAUGHN, Mariah R.;
; APPLICANT: BOROWSKY, Mark L.; ZEBARJADIAN, Yeganeh;
; APPLICANT: RICHARDSON, Thomas W.; MARQUIS, Joseph P.;
; APPLICANT: CHIEN, David; JIN, Pei
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PF-0995 USN
; CURRENT APPLICATION NUMBER: US/10/478,146
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/16634
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/293,665
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/298,712
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/303,418
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/306,967
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/308,183
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/343,007
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/357,675
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/376,988
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 72063274CB1
US-10-478-146-17

Query Match 100.0%; Score 1440; DB 18; Length 1581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGACGCCCATATATCGCCCGGACCGCTATCCCGCCGAGATGCCCGAGTACGGGAGGAG 60
Db 15 ATGGACGCCCATATATCGCCCGGACCGCTATCCCGCCGAGATGCCCGAGTACGGGAGGAG 74
Qy 61 AACCAATCTTCAGTTGATGACAGACATGCTGGAGCAACTCTGATGATCCAGCCCGAA 120
Db 75 AACCAATCTTCAGTTGATGACAGACATGCTGGAGCAACTCTGATGATCCAGCCCGAA 134
Qy 121 GATCCCATCCCTTTCATGATCCAGCATCTTGATAGAGCAACGACAACTGCGCCAGATT 180
Db 135 GATCCCATCCCTTTCATGATCCAGCATCTTGATAGAGCAACGACAACTGCGCCAGATT 194
Qy 181 GTAATATAGTCCACCGCTCAGGAGAAACAACTAGCAATGTGGCTCTGCAAAAT 240
Db 195 GTAATATAGTCCACCGCTCAGGAGAAACAACTAGCAATGTGGCTCTGCAAAAT 254
Qy 241 CTGAACAGCAGTCTCTCCACCTGGAGAACCTGATCTTAATGATTTCTTATAGGCC 300
Db 255 CTGAACAGCAGTCTCTCCACCTGGAGAACCTGATCTTAATGATTTCTTATAGGCC 314
Qy 301 ACCGAGCCAGAGCTTTTATCTCAAGAGGAGACAGTCTCCAGCGCGCTGCTCGTCCAG 360
Db 315 ACCGAGCCAGAGCTTTTATCTCAAGAGGAGAGCAGTCTCCAGCGCGCTGCTCGTCCAG 374
Qy 361 CTGATTCAGGAACCGCTGCTGTAAGAGGATTCATCAAGCAGGGCTGGATCTTGGATGGC 420

Db 375 CTGATTCAGGACGCTGGCTGAGAGGATTCATCAGCAGGCTGGATCTCGATGGC 434
Qy 421 ATCCCTGAGACGGCTGAGGCTCTGAGGATTCAGACCTCTGGGATCACACCCAGACAC 480
Db 435 ATCCCTGAGACGGCTGAGGCTCTGAGGATTCAGACCTCTGGGATCACACCCAGACAC 494
Qy 481 GTCAATGTGCTGAGTCTCCAGACACGCTCTGATCGAGAGAACTTGGGAAAGAAATC 540
Db 495 GTCAATGTGCTGAGTCTCCAGACACGCTCTGATCGAGAGAACTTGGGAAAGAAATC 554
Qy 541 GACCTCAAACTGGAGAGATTTATCACACACCTTTGACTGGCCACCCGATCTGAATC 600
Db 555 GACCTCAAACTGGAGAGATTTATCACACACCTTTGACTGGCCACCCGATCTGAATC 614
Qy 601 CAGAACCGTCTCATGGTCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAACTGCTG 660
Db 615 CAGAACCGTCTCATGGTCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAACTGCTG 674
Qy 661 GAGTATCATAGAACATCTGTCAGGGTCAATTCCTCTACCCCAAAATCCTCAAGTCATC 720
Db 675 GAGTATCATAGAACATCTGTCAGGGTCAATTCCTCTACCCCAAAATCCTCAAGTCATC 734
Qy 721 AGTGTGACCAAGCCATGTGTGGACGCTCTTACCAAGGCTCTGACCTATGTCCAAAGCAAC 780
Db 735 AGTGTGACCAAGCCATGTGTGGACGCTCTTACCAAGGCTCTGACCTATGTCCAAAGCAAC 794
Qy 781 CATCGTACTAATGCCCCGTTTACCCCGAGGGTCTGCTGCTGGGCTCTGGGCACTGGG 840
Db 795 CATCGTACTAATGCCCCGTTTACCCCGAGGGTCTGCTGCTGGGCTCTGGGCACTGGG 854
Qy 841 AAAAGCTGAGGCGGCGCTCTGGCCAGAAATCAGGCTGTCAATGTCTGCTGTGGG 900
Db 855 AAAAGCTGAGGCGGCGCTCTGGCCAGAAATCAGGCTGTCAATGTCTGCTGTGGG 914
Qy 901 CAACTGTGAAAGAGGTGTGGCAGATAGGACACGTTTGGCAGAGCTCATCCAGCCCTTC 960
Db 915 CAACTGTGAAAGAGGTGTGGCAGATAGGACACGTTTGGCAGAGCTCATCCAGCCCTTC 974
Qy 961 TTTGAAAAGGAGATGGCAGTTCTTGACAGCCTCTCATGAAGGTGTGAGCCAGCGCTG 1020
Db 975 TTTGAAAAGGAGATGGCAGTTCTTGACAGCCTCTCATGAAGGTGTGAGCCAGCGCTG 1034
Qy 1021 GACGACGAGACTGCAATCCAGAAAGGCTGGGTGTCTACACGGCTCCGCGGAGCCTGCAC 1080
Db 1035 GACGACGAGACTGCAATCCAGAAAGGCTGGGTGTCTACACGGCTCCGCGGAGCCTGCAC 1094
Qy 1081 CAGGCAACCTGCTGAACCGCTTGGGCTACAAATCCCAACAGGGTGTCTTCTGAAATGTG 1140
Db 1095 CAGGCAACCTGCTGAACCGCTTGGGCTACAAATCCCAACAGGGTGTCTTCTGAAATGTG 1154
Qy 1141 CCAATTCATTCATGAGGCGGTGACTCTGAGAGAAATTCATCCAGTCACTGGGAA 1200
Db 1155 CCAATTCATTCATGAGGCGGTGACTCTGAGAGAAATTCATCCAGTCACTGGGAA 1214
Qy 1201 AGGTACCACTCATGTATCAAGCCACTCCCAACATGAGATCCAGGCTCGCTCTGAG 1260
Db 1215 AGGTACCACTCATGTATCAAGCCACTCCCAACATGAGATCCAGGCTCGCTCTGAG 1274
Qy 1261 AACCCAAAGGATGCTGAGAGCAGTCAAGCTGAAATGGAATCTGTTCTACAGGAATCA 1320
Db 1275 AACCCAAAGGATGCTGAGAGCAGTCAAGCTGAAATGGAATCTGTTCTACAGGAATCA 1334
Qy 1321 GCTGACTTGGAGCAGTTGTATGGGTGGGCCATCACCTCAATGGGAGCAGGACCCATAC 1380
Db 1335 GCTGACTTGGAGCAGTTGTATGGGTGGGCCATCACCTCAATGGGAGCAGGACCCATAC 1394
Qy 1381 ACAGTCTTCGAATACATCGAGAGTGGGATCAATTAATCCCTCCCAAGAAATCCCTGGA 1440
Db 1395 ACAGTCTTCGAATACATCGAGAGTGGGATCAATTAATCCCTCCCAAGAAATCCCTGGA 1454

RESULT 5

US-10-104-047-1657
; Sequence 1657, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1657
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1657

Query Match 81.2%; Score 1170; DB 17; Length 1619;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1272; Conservative 0; Mismatches 0; Indels 92; Gaps 1;
Qy 169 GTGCCAGGATTTGTAATATTAGGTCCACCCGCTCAGGGAACAAACAATAGCAATGTGG 228
Db 148 GTGCCAGGATTTGTAATATTAGGTCCACCCGCTCAGGGAACAAACAATAGCAATGTGG 207
Qy 229 CTCTGCAAAATCTGAAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATGAGTTT 288
Db 208 CTCTGCAAAATCTGAAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATGAGTTT 267
Qy 289 TCCTATACGCCACCGAGCCAGAGGCTTTATCTGCAAGAGAACAGTTCCTCCAGCGCG 348
Db 268 TCCTATACGCCACCGAGCCAGAGGCTTTATCTGCAAGAGAACAGTTCCTCCAGCGCG 327
Qy 349 CTGCTGTCAGCTGATTCAGAAACGCTGTGCTGAAAGAGATTTGCATCAAGCAG 402
Db 328 CTGCTGTCAGCTGATTCAGAAACGCTGTGCTGAAAGAGATTTGCATCAAGCAGTTGGA 387
Qy 403 ----- 402
Db 388 GTTCTTGTAAATAGCGGCTTTTCATCCGCTAATTCAGTATCTGATTCAGTG 447
Qy 403 -----GCTGGATTCGATCGCATCCCTCAGACGGTG 436
Db 448 GTGGTGACATCTGTATCTGCTCTCATGGCTGGATTTGGATGGCATCCCTGAGACGGTG 507
Qy 437 AGCAGGCTCTGAGGATCCAGACCTCTGGGATCACCCAGACACGTCATTTGCTGAGTG 496
Db 508 AGCAGGCTCTGAGGATCCAGACCTCTGGGATCACCCAGACACGTCATTTGCTGAGTG 567
Qy 497 CTCAGACACGGTCTGATCGAGAGAACTTGGGGAAGAGATCCACCTCAAACTGGAG 556
Db 568 CTCAGACACGGTCTGATCGAGAGAACTTGGGGAAGAGATCCACCTCAAACTGGAG 627
Qy 557 AGATTATCACACCACTTTGACTGGCCACCGGATCTGAAATCCAGAACCGTCTCATGG 616
Db 628 AGATTATCACACCACTTTGACTGGCCACCGGATCTGAAATCCAGAACCGTCTCATGG 687
Qy 617 TGCCAGAGGACATCTCAGAGCTGGAGCGGCTCAGAACTCTGGAGTATCATAGGAACA 676
Db 688 TGCCAGAGGACATCTCAGAGCTGGAGCGGCTCAGAACTCTGGAGTATCATAGGAACA 747
Qy 677 TCGTCAGGGTCAATTCCTCTACCCCAAAATCCTCAAGTCAATCAGTGTGACCGCAT 736
Db 748 TCGTCAGGGTCAATTCCTCTACCCCAAAATCCTCAAGTCAATCAGTGTGACCGCAT 807
Qy 737 GTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCAACCATCTACTTAATGCC 796
Db 808 GTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCAACCATCTACTTAATGCC 867
Qy 797 CGTTCAACCCGAGGCTGCTGCTCGGCGCTTGGGAGTGGGAAGTCTCAGGCGCG 856

Mon Mar 21 09:11:06 2005

868 CGTTACCCCGAGGTGCTGCTCTCGGGCTTGGGCGAGTGGGAAAAGTCTGAGGCGG 927
857 CCCTCTGGGCCAGAAATACAGGCTTGTCAATGCTGTGGGCAACTGCTGAAAGAGG 916
928 CCCTCTGGGCCAGAAATACAGGCTTGTCAATGCTGTGGGCAACTGCTGAAAGAGG 987
917 CTGTGGCAGATAGACACGCTTTGGGAGTCTATCCAGGCTTCTTTGAAAAGGAGTGG 976
988 CTGTGGCAGATAGACACGCTTTGGGAGTCTATCCAGGCTTCTTTGAAAAGGAGTGG 1047
977 CAGTTCTGACAGCTCTCATGAGGTGCTGAGCCAGGCTTGGACCAAGGAGTCTGCA 1036
1048 CAGTTCTGACAGCTCTCATGAGGTGCTGAGCCAGGCTTGGACCAAGGAGTCTGCA 1107
1037 TCAGAAAGGCTGGGTGCTACACGGCTCCCGGGGACCTCGACAGGACACCTCTCTGA 1096
1108 TCCAGAAAGGCTGGGTGCTACACGGCTCCCGGGGACCTCGACAGGACACCTCTCTGA 1167
1097 ACCGCTGGGCTACAAATCCCAACAGGCTGTTTCTGTAATGTCATTTGATTCATCA 1156
1168 ACCGCTGGGCTACAAATCCCAACAGGCTGTTTCTGTAATGTCATTTGATTCATCA 1227
1157 TGGAGCGCTGACTCTGAGAAAGATTGATCCAGTCACTGGGGAAGGTACCACTCATGT 1216
1228 TGGAGCGCTGACTCTGAGAAAGATTGATCCAGTCACTGGGGAAGGTACCACTCATGT 1287
1217 ACAAGCCACTCCACATGAGATCCAGGCTCGCTTCTGAGAACCCCAAGGATGCTG 1276
1288 ACAAGCCACTCCACATGAGATCCAGGCTCGCTTCTGAGAACCCCAAGGATGCTG 1347
1277 AAGACAGCTCAAGCTGAAATGGAACCTGTTCTACAGGAATCAGCTGACTGGAGCAGT 1336
1348 AAGACAGCTCAAGCTGAAATGGAACCTGTTCTACAGGAATCAGCTGACTGGAGCAGT 1407
1337 TGTATGGGTGGCCATCAACCTCAATGGGACCGAGGCCATACACAGTCTTCCAAATCA 1396
1408 TGTATGGGTGGCCATCAACCTCAATGGGACCGAGGCCATACACAGTCTTCCAAATCA 1467
1397 TCGAGAGTGGGATCAATTAATCCCTGCCCAAGAAATCCCTCTGA 1440
1468 TCGAGAGTGGGATCAATTAATCCCTGCCCAAGAAATCCCTCTGA 1511

RESULT 6
US-10-165-800-21
Sequence 21, Application US/10165800
Publication No. US20030092116A1
GENERAL INFORMATION:
APPLICANT: Chun, Miyoung
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: No. US20030092116A1el Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Adenylate Kinase, Phospholipid Scramblase-Like, DNA
TITLE OF INVENTION: Fragmentation Factor-Like, Phosphatidylserine Synthase-Like,
TITLE OF INVENTION: and ATPase-Like Molecules and Uses Therefor
FILE REFERENCE: 35800/247838
CURRENT APPLICATION NUMBER: US/10/165,800
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/790,179
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/185,609
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/790,838
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/185,946
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/790,180
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/185,947
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/795,038
PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 60/186,234
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/781,677
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/181,705
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 1452
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (219)...(995)
US-10-165-800-21

Query Match 71.7%; Score 1032.8; DB 14; Length 1452;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 2; Indels 192; Gaps 2;

QY 1 ATGGAAGCCACTATCGGCCCGCCACCGTATCCCGCCGAGATGCCCGAGTACGGGAGAG 60
DB 53 ATGGAAGCCACTATCGGCCCGCCACCGTATCCCGCCGAGATGCCCGAGTACGGGAGAG 112
QY 61 AACCAATCTTCGAGTTGATGAGCAATGCTGGAGCAATCTCTGATCCACAGCCGAGAA 120
DB 113 AACCAATCTTCGAGTTGATGAGCAATGCTGGAGCAATCTCTGATCCACAGCCGAGAA 172
QY 121 GATCCCATCCCTTCATGATCCAGCACTTGCATGAGAAACGACATGTCGCCAGGATT 180
DB 173 GATCCCATCCCTTCATGATCCAGCACTTGCATGAGAAACGACATGTCGCCAGGATT 221
QY 181 GTAATATTAGTTCACCCGCTCAGGGAACAAATAGCAATGTGCTCTGCAAAACAT 240
DB 222 -----GCATGTGGCTCTGCAAAACAT 242
QY 241 CTGAACAGCAGTCTCTCACCCTCGAGAACCTGATCTTAAATGAGTTTCTTATACGGCC 300
DB 243 CTGAACAGCAGTCTCTCACCCTCGAGAACCTGATCTTAAATGAGTTTCTTATACGGCC 302
QY 301 ACCGAAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCCCGAGCGCTGCTGCTCCAG 360
DB 303 ACCGAAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCCCGAGCGCTGCTGCTCCAG 362
QY 361 CTGATTCAGGAAGCGCTGCTGAGAGGATTCATCAAGAGGATTCATCAAGAGGCTGGAATCTGATGCG 420
DB 363 CTGATTCAGGAAGCGCTGCTGAGAGGATTCATCAAGAGGATTCATCAAGAGGCTGGAATCTGATGCG 422
QY 421 ATCCCTGAGACGCTGAGCAGGCTCTGAGGATTCAGACCTTGGGATCACACCCAGACAC 480
DB 423 ATCCCTGAGACGCTGAGCAGGCTCTGAGGATTCAGACCTTGGGATCACACCCAGACAC 482
QY 481 GTCAATTTGTGATGCTCTCCAGACGCTCTGATCGAGAGAACTTGGGGAGAGAAATC 540
DB 483 GTCAATTTGTGATGCTCTCCAGACGCTCTGATCGAGAGAACTTGGGGAGAGAAATC 542
QY 541 GACCCCTCAAACTGGAGAGATTTATCAACAACCTTTGATCTGGCCACCCGAAATCTGAATC 600
DB 543 GACCCCTCAAACTGGAGAGATTTATCAACAACCTTTGATCTGGCCACCCGAAATCTGAATC 602
QY 601 CAGAACCGTCTCATGTTGGCCAGAGGACATCTCAGAGCTGGAGACGCTCAGAAACTGCTG 660
DB 603 CAGAACCGTCTCATGTTGGCCAGAGGACATCTCAGAGCTGGAGACGCTCAGAAACTGCTG 662
QY 661 GAGTATCATAGGAACATCTGTCAGGCTCATTCCTCTTACCCAAAATCTCTCAAGTCATC 720
DB 663 GAGTATCATAGGAACATCTGTCAGGCTCATTCCTCTTACCCAAAATCTCTCAAGTCATC 722
QY 721 AGTGTGACCAAGCCATGTGTGAGGCTCTTACAGGCTCTGACCTATGTCCTCAAGCAAC 780
DB 723 AGTGTGACCAAGCCATGTGTGAGGCTCTTACAGGCTCTGACCTATGTCCTCAAGCAAC 782


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QY 781 CATGCTACTAATCCCGCTTCAACCCGAGGGTGTGCTGCTCGGGCTGTGGCGAGTGGG 840
Db CATGCTACTAATCCCGCTTCAACCCGAGGGTGTGCTGCTCGGGCTGTGGCGAGTGGG 842
QY 841 AAAAGTCTGAGCGCGCCCTCTCGCCGAGAAATACAGGCTTGTCAATGTCTGCTGTGGG 900
Db AAAAGTCTGAGCGCGCCCTCTCGCCGAGAAATACAGGCTTGTCAATGTCTGCTGTGGG 902
QY 901 CAATGCTGAAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 960
Db CAATGCTGAAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 962
QY 961 TTTGAAAAGGAGATGCGAGTTCTTGACAGCTCTCATGAAGTGTCTGAGCGAGCTG 1020
Db TTTGAAAAGGAGATGCG----- 978
QY 1021 GACCAGCAGGACTGCATCCAGAAAGGCTGGGTGCTACACGGCGTCCCGGGACCTCGAC 1080
Db 979 ----- 978
QY 1081 CAGGCACACTGCTGAACCGCTGGGCTACAAATCCCAACAGGGTGTCTTCTGGAATGTG 1140
Db 979 -----CAGGGTGTCTTCTGGAATGTG 1000
QY 1141 CCATTGTGATTCATCATGAGCGGCTGACTCTGAGNAGAAATGATCCAGTCACTGGGGAA 1200
Db CCATTGTGATTCATCATGAGCGGCTGACTCTGAGNAGAAATGATCCAGTCACTGGGGAA 1060
QY 1201 AGGTACCACTCATGTACAGCCACCTCCACATGAGAGATCCAGGCTCGCTCTGCGAG 1260
Db AGGTACCACTCATGTACAGCCACCTCCACATGAGAGATCCAGGCTCGCTCTGCGAG 1120
QY 1261 AACCCAAAGAGTGTGAAGAGCAGGTCAAGCTGAAATGGAATGGAACCTGTCTACAGGAATCA 1320
Db 1121 AACCCAAAGAGTGTGAAGAGCAGGTCAAGCTGAAATGGAACCTGTCTACAGGAATCA 1180
QY 1321 GCTGACTTGGAGCAGTGTGATGGTGGGCTCGGCATCACCTCAATGGGAGCAGGACCCATAC 1380
Db 1181 GCTGACTTGGAGCAGTGTGATGGTGGGCTCGGCATCACCTCAATGGGAGCAGGACCCATAC 1240
QY 1381 ACAGTCTTCGAATACATCGAGAGTGGGATCAATTCCTGCGCCGAGAAATCCCTTGA 1440
Db 1241 ACAGTCTTCGAATACATCGAGAGTGGGATCAATTCCTGCGCCGAGAAATCCCTTGA 1300

RESULT 7
US-09-764-868-257
; Sequence 257, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1163)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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; LOCATION: (1181)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1191)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1193)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1203)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1218)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-868-257

Query Match 71.4%; Score 1027.6; DB 9; Length 1223;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 10; Indels 43; Gaps 8;

QY 1 ATGGAACCCACTATCGCCCGCACCGTATCCCCCGGAGATGCCCGAGATGCCCGAGTACGGGAGGAG 60
Db 6 ATGGAACCCACTATCGCCCGCACCGTATCCCCCGGAGAGTCCCATGCCCTTCATGATCCAG 63
QY 61 AACCAACATCTTCCGAGTTGATG-----CAG 84
Db 64 AACCAACATCTTCCGAGTTGATG-----CAG 84
QY 85 AACATGCTGGAGCACTCTCTGATCCACAGCCCGAAGATCCCATGCCCTTCATGATCCAG 144
Db 124 AACATGCTGGAGCACTCTCTGATCCACAGCCCGAAGATCCCATGCCCTTCATGATCCAG 183
QY 145 CACTGTGATAGAGACAACGACAATGTGCCAGGATTTGTAATATTAGTCTCCACCGCCCTCA 204
Db 184 CACTGTGATAGAGACAACGACAATGTGCCAGGATTTGTAATATTAGTCTCCACCGCCCTCA 243
QY 205 GGGAAACAAACAAATAGCAATGTGCTGCAAAACATCTG- AACAGCAGTCTCCCTCAGCCT 263
Db 244 GGGAAACAAACAAATAGCAATGTGCTGCAAAACATCTG- AACAGCAGTCTCCCTCAGCCT 303
QY 264 GGA- GAACCTGATCTTAATGAGTTTTCCTATAGCGCCACCGAGCCAG- AAGGCTTTAT 321
Db 304 GGA- GAACCTGATCTTAATGAGTTTTCCTATAGCGCCACCGAGCCAG- AAGGCTTTAT 363
QY 322 CTGCAAGGAGAGACAGTTCCACGCGCTGCTGCTCAGCTGATTCAGGAACGCTGGCT 381
Db 364 CTGCAAGGAGAGACAGTTCCACGCGCTGCTGCTCAGCTGATTCAGGAACGCTGGCT 423
QY 382 GAAGAGGATTCATCAAGCAGGGCTGGATTTCTGGATGGCATCCCTGAGAGCGGTGAGCAG 441
Db 424 GAAGAGGATTCATCAAGCAGGGCTGGATTTCTGGATGGCATCCCTGAGAGCGGTGAGCAG 482
QY 442 GCTCTGAGGATTCAGACCCCTGGGGATCACACCCAGACAGCTCATGCTGAGTGTCCA 501
Db 483 GCTCTGAGGATTCAGACCCCTGGGGATCACACCCAGACAGCTCATGCTGAGTGTCCA 542
QY 502 GACAGGCTCTGATCGAGAGAACTTGGGGAAGAGAAATCGACCTCAAACTGGAGAGATT 561
Db 543 GACAGGCTCTGATCGAGAGAACTTGGGGAAGAGAAATCGACCTCAAACTGGAGAGATT 602
QY 562 TATCACCACTTTGATGGGCCACCCGAAATCCAGAACTCCAGAACCTCTCATGTTGGCCA 621
Db 603 TATCACCACTTTGATGGGCCACCCGAAATCCAGAACTCCAGAACCTCTCATGTTGGCCA 662
QY 622 GAGGACATCTCAGAGTGGAGACGGCTCAGAACTGCTGGAGTATCATAGGACATCTGTC 681
Db 663 GAGGACATCTCAGAGTGGAGACGGCTCAGAACTGCTGGAGTATCATAGGACATCTGTC 722
QY 682 AGGTCATCTCCCTACCCCAAAATCTCAAACTCATAGTCTGCTGACAGCCATGTGTG 741
Db 723 AGGTCATCTCCCTACCCCAAAATCTCAAACTCATAGTCTGCTGACAGCCATGTGTG 782
QY 742 GACGTCTTACAGGCTCTGACTTATGTCCAAAGCAACCATCTGTAATGCCCGCTTC 801
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Db 783 GAGCTCTTCTACAGGCTCTGACCTATGTCTAAAGCAACCATCGTACTAATGCCCGGTC 842
Qy 802 ACCCGAGGCTGCTGCTCGGCGCTGTGGGCAAGTGGGAAAGTCTGAGGCGCGCCCTC 861
Db 843 ACCCGAGGCTGCTGCTCGGCGCTGTGGGCAAGTGGGAAAGTCTGAGGCGCGCCCTC 902
Qy 862 CTGCCCCAGAAATACAGGCTTGTCAATGTCTGTGTGGGCAACTGTGAAAGAGGCTGTG 921
Db 903 CTGCCCCAGAAATACAGGCTTGTCAATGTCTGTGTGGGCAACTGTGAAAGAGGCTGTG 962
Qy 922 GCAGATAGGACCACTTTGGGAGCTCATCCAGCCCTTCTTCAAAAGAGAGATGGCAGTT 981
Db 963 GCAGATAGGACCACTTTGGGAGCTCATCCAGCCCTTCTTCAAAAGAGAGATGGCAGTT 1022
Qy 982 CTTGACAGCTTCTCATGAAGGCTGTGAGCGAGCGCTGAGCGAGCGCTGAGCGAGCGCTGATCCAG 1041
Db 1023 CTTGACAGCTTCTCATGAAGGCTGTGAGCGAGCGCTGAGCGAGCGCTGAGCGAGCGCTGATCCAG 1082
Qy 1042 AAGGCTGGGTGTACAGCGGCTCCCGGAGCGCTGAGCGAGCGCTGAGCGAGCGCTGATCCAG 1101
Db 1083 AAGGCTGGGTGTACAGCGGCTCCCGGAGCGCTGAGCGAGCGCTGAGCGAGCGCTGATCCAG 1142
Qy 1102 CTGGGCTACAA-TCCCAACAGGCTGTTTCTTCTGAATGTGCAATTTGATTCATATGGA 1160
Db 1143 CTGGGCTACAA-TCCCAACAGGCTGTTTCTTCTGAATGTGCAATTTGATTCATATGGA 1202
Qy 1161 GCGGCT 1166
Db 1203 NCGGCT 1208

RESULT 8

US-10-311-034-51
; Sequence 51, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GRETHER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.

; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/219,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-08-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 51
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 621293CB1
US-10-311-034-51

Query Match 60.3%; Score 868; DB 17; Length 995;
Best Local Similarity 100.0%; Pred. No. 1.5e-269; Indels 0; Gaps 0;
Matches 868; Conservative 0; Mismatches 0;

Qy 573 CTTTGACTGGCCACCCGAATCTGAAATCCAGAACCGTCTCATGTGTCCAGAGGACATCTC 632
Db 3 CTTTGACTGGCCACCCGAATCTGAAATCCAGAACCGTCTCATGTGTCCAGAGGACATCTC 62
Qy 633 AGAGCTGGAGCGGCTCAGAACTGCTGGAGTATCATAGGAACATCTCAGGCGTCATTCC 692
Db 63 AGAGCTGGAGCGGCTCAGAACTGCTGGAGTATCATAGGAACATCTCAGGCGTCATTCC 122
Qy 693 CTCCTACCCCAAAATCCTCAAAAGTCATCAGTGTGTCAGCAGCCATGTGTGAGAGCTTCTA 752
Db 123 CTCCTACCCCAAAATCCTCAAAAGTCATCAGTGTGTCAGCAGCCATGTGTGAGAGCTTCTA 182
Qy 753 CCAGGCTCTGACTATGTCCAAAGCAACATCTGACTACTTAATGCCCGTTTACCCGAGGCT 812
Db 183 CCAGGCTCTGACTATGTCCAAAGCAACATCTGACTACTTAATGCCCGTTTACCCGAGGCT 242
Qy 813 GCTGCTGCTCGGCGCTGTGGGAGTGGGAAAGTCTGAGCGCGCCCTCTCTGGGCCAGAA 872
Db 243 GCTGCTGCTCGGCGCTGTGGGAGTGGGAAAGTCTGAGCGCGCCCTCTCTGGGCCAGAA 302
Qy 873 ATACAGGCTTGTCAATGTCTGTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGATAGAC 932
Db 303 ATACAGGCTTGTCAATGTCTGTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGATAGAC 362
Qy 933 CAGCTTTGGCGAGCTCATCCAGCCCTTCTTGAAGAGAGATGGCAGTTTCTTGACAGCT 992
Db 363 CAGCTTTGGCGAGCTCATCCAGCCCTTCTTGAAGAGAGATGGCAGTTTCTTGACAGCT 422
Qy 993 CCTCATGAAGGCTGTGAGCGCGCTGAGCAGAGGACTGATCCAGAAAGGCTGGGT 1052
Db 423 CCTCATGAAGGCTGTGAGCGCGCTGAGCAGAGGACTGATCCAGAAAGGCTGGGT 482
Qy 1053 GCTACAGGCTCCCGGAGCGCTGAGCAGGACACCTGCTGAAACCGGCTGGGCTACAA 1112
Db 483 GCTACAGGCTCCCGGAGCGCTGAGCAGGAGCTGAGCAGGACACCTGCTGAAACCGGCTGGGCTACAA 542
Qy 1113 TCCCAACAGGCTGTTTCTTCTGAAATGTGCCATTTTCAATTCATGAGGCGGTGACTCT 1172
Db 543 TCCCAACAGGCTGTTTCTTCTGAAATGTGCCATTTTCAATTCATGAGGCGGTGACTCT 602
Qy 1173 GAGAAGAAATTGATCCAGTCTGAGTGGGAAAGGTACCACTCATGTACAAGCACCTCCAC 1232
Db 603 GAGAAGAAATTGATCCAGTCTGAGTGGGAAAGGTACCACTCATGTACAAGCACCTCCAC 662
Qy 1233 CATGGAGATCCAGGCTCGCCCTCTGTCAGAAACCCAAAGGATGCTGAAGAGAGCTCAAGCT 1292
Db 663 CATGGAGATCCAGGCTCGCCCTCTGTCAGAAACCCAAAGGATGCTGAAGAGAGCTCAAGCT 722
Qy 1293 GAAAATGACCTGTTTCTACAGGAATCAGTGTGAGCAGTGTGATGGGTGGGCGCAT 1352

Db 723 GAATGACCTGTTCTACAGGAATCAGCTGACTTGGAGCAGTTGTATGGTTCGGCCAT 782
Qy 1353 CACCTCTAATGGGACAGGACCCATACACAGCTCTTGAATACATGAGAGTGGATCAT 1412
Db 783 CACCTCTAATGGGACAGGACCCATACACAGCTCTTGAATACATGAGAGTGGATCAT 842
Qy 1413 TAATCCCTGCCCAAGAAATCCCTGA 1440
Db 843 TAATCCCTGCCCAAGAAATCCCTGA 870

RESULT 9

US-10-098-841-257
; Sequence 257, Application US/10098841
; Publication No. US20020197679A1

GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Dmanac, Radje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_fl_genes Version 1.0
; SEQ ID NO 257

; LENGTH: 1778
; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (63)...(1778)

US-10-098-841-257

Query Match

Best Local Similarity 52.8%; Score 761; DB 13; Length 1778;
Matches 803; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 220 GCAATGTGGCTCTGCAAAATCTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTA 279
Db 147 GCAATGTGGCTCTGCAAAATCTGAACAGCAGTCTCTCAACCTGGAGAACCTGATCTTA 206
Qy 280 AATGAGTTTCTATACGGCCACGAGCCAGAGGCTTTATTCGAAAGGAGACAGTT 339
Db 207 AATGAGTTTCTATACGGCCACGAGCCAGAGGCTTTATTCGAAAGGAGACAGTT 266
Qy 340 CCCAGCGCTGCTGCTCCAGCTGATTCAGGACGCTGCTGAGAGGATTCATCAAG 399
Db 267 CCCAGCGCTGCTGCTCCAGCTGATTCAGGACGCTGCTGAGAGGATTCATCAAG 326
Qy 400 CAGGCTGATTTCTGATGTCATCCCTGAGACGGCTGAGCAGGCTCTGAGGATCCAGACC 459
Db 327 CAGGCTGATTTCTGATGTCATCCCTGAGACGGCTGAGCAGGCTCTGAGGATCCAGACC 386

Qy 460 CTGGGATCACCCAGACAGCTCATTTGTGCTGAGTGTCTCAGACAGGTCCTGATCGAG 519
Db 387 CTGGGATCACCCAGACAGCTCATTTGTGCTGAGTGTCTCAGACAGGTCCTGATCGAG 446
Qy 520 AGAACTTGGGAGAGAGATCGACCCCTCAAACCTGGAGAGATTTATCACACACCTTTGAC 579
Db 447 AGAACTTGGGAGAGAGATCGACCCCTCAAACCTGGAGAGATTTATCACACACCTTTGAC 506
Qy 580 TGGCCACCCGAAATCTGAAATCCAGAACCGTCTCATGTTGCCAGAGGACATCTCAGAGCTG 639
Db 507 TGGCCACCCGAAATCTGAAATCCAGAACCGTCTCATGTTGCCAGAGGACATCTCAGAGCTG 566
Qy 640 GAGACGGCTCAGAAATCTGCTGGAGTATCATAGGAACATGTCAGGGTCATTTCCCTCTAC 699
Db 567 GAGACGGCTCAGAAATCTGCTGGAGTATCATAGGAACATGTCAGGGTCATTTCCCTCTAC 626
Qy 700 CCCAAATCTCAAAGTCAATCAGTGTGACCAAGCCATGTGTGGACGTCTTCTACCAAGCT 759
Db 627 CCCAAATCTCAAAGTCAATCAGTGTGACCAAGCCATGTGTGGACGTCTTCTACCAAGCT 686
Qy 760 CTGACCTATGTCCTAAAGCAACCATCGTACTTAATGCCCGTTTCAACCCGAGGCTGCTG 819
Db 687 CTGACCTATGTCCTAAAGCAACCATCGTACTTAATGCCCGTTTCAACCCGAGGCTGCTG 746
Qy 820 CTCGGGCTGTGGGAGTGGGAAAGTCTGTCAGGGCCGCTCTCTGGGCCAGAAATACAGG 879
Db 747 CTCGGGCTGTGGGAGTGGGAAAGTCTGTCAGGGCCGCTCTCTGGGCCAGAAATACAGG 806
Qy 880 CTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGATAGGACCAAGCTTT 939
Db 807 CTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGATAGGACCAAGCTTT 866
Qy 940 GGGAGCTCATCCAGCCCTCTTTGAAAGAGGATGCGAGTCTCTGACAGCTCTCTCATG 999
Db 867 GGGAGCTCATCCAGCCCTCTTTGAAAGAGGATGCGAGAGGAGGAGGAGGAGGAGGAGG 926
Qy 1000 AAGTGTGAGCCAGCGCTGAGACAGCAGGACTGCAATCCAGAAAGGCTGGGTGCTACAC 1059
Db 927 GGAACAGTGGAAATTCAGCTTCCGAAACATGCTCCCTGCAACAGAGGACCTGCCCTG 986
Qy 1060 GGGTCCCGGGACCTCGACAGGACACCTG 1092
Db 987 CTGAACTGGAGACATGCTGTATCCCTG 1019

RESULT 10

US-10-165-800-23
; Sequence 23, Application US/10165800
; Publication No. US20030092116A1
; GENERAL INFORMATION:
; APPLICANT: Chun, Miyoung
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; TITLE OF INVENTION: No. US20030092116A1el Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Adenylate Kinase, Phospholipid Scramblase-Like, DNA
; TITLE OF INVENTION: Fragmentation Factor-Like, Phosphatidylserine Synthase-Like,
; FILE REFERENCE: 35800/247838
; CURRENT APPLICATION NUMBER: US/10/165,800
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/790,179
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/185,609
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/790,838
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/185,946
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/790,180
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/185,947

Mon Mar 21 09:11:06 2005

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; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/795,038
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186,234
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/781,677
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/181,705
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-165-800-23

Query Match      52.8%; Score 759.8; DB 14; Length 774;
Best Local Similarity 99.7%; Pred. No. 1.4e-234;
Matches 761; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 217 ATAGCAATGTGGCTCTGCAACATCTGAACAGCAGTCTCTCCTCGGTGGAGAACCTGATC 276
Db 1 ATGGCAATGTGGCTCTGCAACATCTGAACAGCAGTCTCTCCTCGGTGGAGAACCTGATC 60

QY 277 TTAATAGTATTTCTATACGGCCACCGAAGCCAGAGGCTTTATCTGCAAGGAGACA 336
Db 61 TTAATAGTATTTCTATACGGCCACCGAAGCCAGAGGCTTTATCTGCAAGGAGACA 120

QY 337 GTTCCAGCGCTCTCGTCCAGCTGATTGAGAAAGCGCTTGGTGAAGAGGATTGATC 396
Db 121 GTTCCAGCGCTCTCGTCCAGCTGATTGAGAAAGCGCTTGGTGAAGAGGATTGATC 180

QY 397 AAGCAGGGCTGATTTGATGGGATCCTGAGAGCGTGGAGCGGCTCTGAGATCCAG 456
Db 181 AAGCAGGGCTGATTTGATGGGATCCTGAGAGCGTGGAGCGGCTCTGAGATCCAG 240

QY 457 ACCCTGGGATCACACCCAGACACCTGATTGTGCTGAGTGTCCAGACACCGTCTGATC 516
Db 241 ACCCTGGGATCACACCCAGACACCTGATTGTGCTGAGTGTCCAGACACCGTCTGATC 300

QY 517 GAGAGAAATTTGGGGAAGAGATTCGACCTCAAACTGAGAGATTATCACACACCTTT 576
Db 301 GAGAGAAATTTGGGGAAGAGATTCGACCTCAAACTGAGAGATTATCACACACCTTT 360

QY 577 GACTGGCCACCGAATCTGAATCCAGAACCTCTCATGCTGCCAGAGGACATCTCAGAG 636
Db 361 GACTGGCCACCGAATCTGAATCCAGAACCTCTCATGCTGCCAGAGGACATCTCAGAG 420

QY 637 CTGGAGACGGCTCAGAAACTGTGGAGTATCATAGAAACATCGTCAGGGTCATTCCTCC 696
Db 421 CTGGAGACGGCTCAGAAACTGTGGAGTATCATAGAAACATCGTCAGGGTCATTCCTCC 480

QY 697 TACCCCAAAATCTCAAGTCATCATGCTGACAGCCCATGTGTGGACGCTTTCTACCAAG 756
Db 481 TACCCCAAAATCTCAAGTCATCATGCTGACAGCCCATGTGTGGACGCTTTCTACCAAG 540

QY 757 GCTCTGACCTATGTCCAAAGCAACCATCTGTAATGCCCGGTTCAACCCGAGGGTGTG 816
Db 541 GCTCTGACCTATGTCCAAAGCAACCATCTGTAATGCCCGGTTCAACCCGAGGGTGTG 600

QY 817 CTGCTCGGGCTGTGGGAGTGGGAAGTCTGCAGCGCCCTCTCGGCCAGAAATAC 876
Db 601 CTGCTCGGGCTGTGGGAGTGGGAAGTCTGCAGCGCCCTCTCGGCCAGAAATAC 660

QY 877 AGGCTGTCAATGTCTGCTGGGCAACTGTCTGAAGAGGCTGTGGCAGATAGGACAG 936
Db 661 AGGCTGTCAATGTCTGCTGGGCAACTGTCTGAAGAGGCTGTGGCAGATAGGACAG 720

QY 937 TTTGGCAGCTCATCCAGCCCTCTTTTGAAGAGGATGGCAG 979
Db 721 TTTGGCAGCTCATCCAGCCCTCTTTTGAAGAGGATGGCAG 763
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RESULT 11
US-09-918-995-16667
; Sequence 16667, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16667
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-16667

Query Match      28.3%; Score 407; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.4e-120;
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 CGCTGCTCGTCCAGCTGATTCAGGAACGCTTGGCTGAAGAGGATTGCATCAAGCAGGCT 406
Db 1 CGCTGCTCGTCCAGCTGATTCAGGAACGCTTGGCTGAAGAGGATTGCATCAAGCAGGCT 60

QY 407 GGATTTCTGGATGGCATCCCTGAGACGGTGTGAGAGGCTCTGAGATCCAGACCTGGGGA 466
Db 61 GGATTTCTGGATGGCATCCCTGAGACGGTGTGAGAGGCTCTGAGATCCAGACCTGGGGA 120

QY 467 TCACACCCAGACACGTCATTTGCTGAGTGTCCAGACACGCTCTGATCGAGAGAACT 526
Db 121 TCACACCCAGACACGTCATTTGCTGAGTGTCCAGACACGCTCTGATCGAGAGAACT 180

QY 527 TGGGGAAGAGAAATCGAACCTCAAACTGGAGAGATTATTCACACACCTTTGACTGGCCAC 586
Db 181 TGGGGAAGAGAAATCGAACCTCAAACTGGAGAGATTATTCACACACCTTTGACTGGCCAC 240

QY 587 CCGAATCTGAAATCCAGAACCGTCTCATGCTGCCAGAGGACATCTCAGAGCTGGAGACGG 646
Db 241 CCGAATCTGAAATCCAGAACCGTCTCATGCTGCCAGAGGACATCTCAGAGCTGGAGACGG 300

QY 647 CTGAGAACTGTCTGGAGTATCATAGAAACATCGTCAGGGTCATTCCTCTACCCCAAAA 706
Db 301 CTGAGAACTGTCTGGAGTATCATAGAAACATCGTCAGGGTCATTCCTCTACCCCAAAA 360

QY 707 TCCTCAAAAGTCATCAGTGTGACCCAGCCATGTGTGGACGCTTTCTAC 753
Db 361 TCCTCAAAAGTCATCAGTGTGACCCAGCCATGTGTGGACGCTTTCTAC 407

RESULT 12
US-09-918-995-29164
; Sequence 29164, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29164
; LENGTH: 447
; TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(447)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29164

Query Match 25.5%; Score 366.6; DB 10; Length 447;
Best Local Similarity 97.6%; Pred. No. 1.7e-107;
Matches 372; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1060 GGCGTCCCGGACCTCGACAGGACACCTGCTGAACCGCTGGGCTCAATCCCAAC 1119
DB 51 GCCGGGTGCGGGACCTCGACAGGACACCTGCTGAATCGGCTGGTCAATCCCAAC 110
QY 1120 AGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAGA 1179
DB 111 AGGGAGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAGA 170
QY 1180 ATTGATCCAGTCACTGGGGAAAGGTACACCTCATGTACAAGCCACCTCCACCATGGAG 1239
DB 171 ATTGATCCAGTCACTGGGGAAAGGTACACCTCATGTACAAGCCACCTCCACCATGGAG 230
QY 1240 ATCCAGGCTCGCCTCTCGAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAGATG 1299
DB 231 ATCCAGGCTCGCCTCTCGAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAGATG 290
QY 1300 GACCTGTTCACAGAACTCAGCTGACTTTGAGAGAGTTGATGGTGGGCTACCCCTC 1359
DB 291 GACCTGTTCACAGAACTCAGCTGACTTTGAGAGAGTTGATGGTGGGCTACCCCTC 350
QY 1360 AATGGGACAGGACCCATACACAGTCTTCGATACATCGAGTGGGATCAATATCC 1419
DB 351 AATGGGACAGGACCCATACACAGTCTTCGATACATCGAGTGGGATCAATATCC 410
QY 1420 CTGCCCAAGAAATCCCTGA 1440
DB 411 CTGCCCAAGAAATCCCTGA 431

RESULT 13
US-09-764-868-255
Sequence 255, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 255
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-868-255

Query Match 22.4%; Score 322; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.8e-93;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1119 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 1178
DB 58 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 117
QY 1179 AATTGATCCAGTCACTGGGGAAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 1238
DB 118 AATTGATCCAGTCACTGGGGAAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 177
QY 1239 GATCCAGGCTCGCCTCTCGAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAT 1298

DB 178 GATCCAGGCTCGCCTCTCGAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAT 237
QY 1299 GGACCTGTTCACAGGAACTCAGCTGACTTTGAGAGAGGTGATCGGTCGCCCATCACCT 1358
DB 238 GGACCTGTTCACAGGAACTCAGCTGACTTTGAGAGAGGTGATCGGTCGCCCATCACCT 297
QY 1359 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 1418
DB 298 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 357
QY 1419 CTGCCCAAGAAATCCCTGA 1440
DB 358 CTGCCCAAGAAATCCCTGA 379

RESULT 14
US-09-764-868-566
Sequence 566, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 566
LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-566

Query Match 22.4%; Score 322; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.8e-93;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1119 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 1178
DB 59 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 118
QY 1179 AATTGATCCAGTCACTGGGGAAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 1238
DB 119 AATTGATCCAGTCACTGGGGAAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 178
QY 1239 GATCCAGGCTCGCCTCTCGAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAT 1298
DB 179 GATCCAGGCTCGCCTCTCGAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAT 238
QY 1299 GGACCTGTTCACAGGAACTCAGCTGACTTTGAGAGAGGTGATGGTGGGCTACACCT 1358
DB 239 GGACCTGTTCACAGGAACTCAGCTGACTTTGAGAGAGGTGATGGTGGGCTACACCT 298
QY 1359 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 1418
DB 299 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 358
QY 1419 CTGCCCAAGAAATCCCTGA 1440
DB 359 CTGCCCAAGAAATCCCTGA 380

RESULT 15
US-10-141-634-3
Sequence 3, Application US/10141634
Publication No. US2003008365A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan

Mon Mar 21 09:11:06 2005

```

; APPLICANT: Xie, Qiongsu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20030008365A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 285
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-634-3

Query Match      19,8t; Score 285; DB 14; Length 285;
Best Local Similarity 100.0t; Pred. No. 3.4e-81;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1156 ATGGAGCGGCTGACTCTGAGAAGAAATTGATCCAGTCACTGGGGAAGGTACCACTCATG 1215
Db      1 ATGGAGCGGCTGACTCTGAGAAGAAATTGATCCAGTCACTGGGGAAGGTACCACTCATG 60

QY      1216 TACAAGCCACTCCCAACCATGGATCCAGGCTCGCCTCTGCGAAGACCCCAAGGATGCT 1275
Db      61 TACAAGCCACTCCCAACCATGGATCCAGGCTCGCCTCTGCGAAGACCCCAAGGATGCT 120

QY      1276 GAAGAGCAGGTCAAGCTGAAATGGACCTGTTCTACAGGAATCTCAGCTGACTTGGAGCAG 1335
Db      121 GAAGAGCAGGTCAAGCTGAAATGGACCTGTTCTACAGGAATCTCAGCTGACTTGGAGCAG 180

QY      1336 TTGTATGGGTGGGCCATCACCTCAATGGGACAGGACCCCATACACAGTCTTCGAATAC 1395
Db      181 TTGTATGGGTGGGCCATCACCTCAATGGGACAGGACCCCATACACAGTCTTCGAATAC 240

QY      1396 ATCGAGAGTGGGATCATTAATCCCTGCGCCCAAGAAATCCCTGA 1440
Db      241 ATCGAGAGTGGGATCATTAATCCCTGCGCCCAAGAAATCCCTGA 285

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Search completed: March 20, 2005, 01:40:30
Job time : 815 secs

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 20:32:04 ; Search time 276 Seconds
(without alignments)
8537.096 Million cell updates/sec

Title: US-10-798-773-1

Perfect score: 1440
Sequence: 1 atggagccactatcgcccc.....tgcccaagaataccctccta 1440

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgm2_6/prodata/1/ina/PTUS.COMB.seq:*

6: /cgm2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	285	19.8	285	4	US-10-141-634-3
3	111	7.7	264	4	US-09-513-999C-3495
C 4	66.4	4.6	747	4	US-09-252-991A-4328
C 5	66.4	4.6	792	4	US-09-252-991A-4185
6	66.4	4.6	849	4	US-09-252-991A-4526
7	66.4	4.6	1002	4	US-09-252-991A-4423
8	63.2	4.4	678	4	US-09-489-039A-5541
9	56.8	3.9	854	2	US-08-829-027-2
10	56.8	3.9	854	2	US-09-225-366-2
11	56.8	3.9	1751	3	US-09-149-476-68
12	41.8	2.9	1866	4	US-09-489-039A-3207
13	41.8	2.9	2237	4	US-09-949-016-5838
14	40.4	2.8	4403765	3	US-09-103-840A-2
15	40.4	2.8	4411529	3	US-09-103-840A-1
C 16	40	2.8	1686	4	US-09-252-991A-5746
C 17	40	2.8	1761	4	US-09-252-991A-5762
18	40	2.8	1890	4	US-09-252-991A-5694
19	40	2.8	6651	4	US-09-902-540-4944
20	40	2.8	30780	4	US-09-902-540-1243
21	39.8	2.8	852	1	US-08-879-561-6
22	39.8	2.8	1070	3	US-09-118-442-16
23	39.8	2.8	1070	3	US-09-677-064-16
24	39.8	2.8	1082	3	US-09-118-442-28
25	39.8	2.8	1082	3	US-09-677-064-28
26	39.6	2.8	1206	4	US-09-252-991A-9058
27	39.6	2.8	1362	4	US-09-252-991A-9224

C 28	39.2	2.7	56523	4	US-09-949-016-14297	Sequence 14297, A
C 29	39.2	2.7	61042	4	US-09-949-016-13224	Sequence 13224, A
C 30	39.2	2.7	61735	4	US-09-949-016-12064	Sequence 12064, A
C 31	39	2.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 32	39	2.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
33	38.8	2.7	1008	4	US-09-252-991A-5442	Sequence 5442, Ap
34	38.8	2.7	2493	4	US-09-252-991A-5433	Sequence 5433, Ap
35	38.8	2.7	6424	4	US-09-902-540-584	Sequence 584, App
36	38.6	2.7	4245	4	US-09-902-540-3647	Sequence 3647, Ap
37	38.6	2.7	16563	4	US-09-902-540-2000	Sequence 2000, Ap
C 38	38.6	2.7	16844	4	US-09-902-540-1176	Sequence 1176, Ap
39	38.4	2.7	693	4	US-09-252-991A-7207	Sequence 7207, Ap
40	38.4	2.7	699	4	US-09-252-991A-7147	Sequence 7147, Ap
41	38.4	2.7	2057	4	US-09-902-540-4222	Sequence 4222, Ap
42	38.4	2.7	26289	4	US-09-902-540-1210	Sequence 1210, Ap
43	38.2	2.7	4941	4	US-09-902-540-7814	Sequence 7814, Ap
C 44	38.2	2.7	7650	4	US-09-902-540-779	Sequence 779, App
45	38	2.6	4179	4	US-09-774-528-122	Sequence 122, App

ALIGNMENTS

RESULT 1

US-10-141-634-1
; Sequence 1, Application US/10141634
; Patent No. 6734010

GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan

; APPLICANT: Xie, Qiongshu

; APPLICANT: Abuein, Alejandro

; APPLICANT: Walker, D. Wade

; TITLE OF INVENTION: No. 6734010el Human Kinases and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0344-USA

; CURRENT APPLICATION NUMBER: US/10/141.634

; PRIOR FILING DATE: 2002-05-08

; PRIOR APPLICATION NUMBER: US 60/289,727

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1440

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-141-634-1

Query Match	100.0%	Score 1440;	DB 4;	Length 1440;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGCGCCACTATCGCCCGCCGACCGCTATCCCCCGAGATGCCCGAGATGCCCGAGTGGCGGAGGAG 60		
Db	1	ATGGAGCGCCACTATCGCCCGCCGACCGCTATCCCCCGAGATGCCCGAGTGGCGGAGGAG 60		
QY	61	AACCAATCTTCGAGTTGATGCAGAACATGCTGGAGCACTCTGAGCACTCTGATCCACCGCGAA 120		
Db	61	AACCAATCTTCGAGTTGATGCAGAACATGCTGGAGCACTCTGATCCACCGCGCGAA 120		
QY	121	GATCCATCCCTTCATGATCCAGCATCTTGATAGAGCAACAGCAATAGCAATGTGGCTCTGCAAGATT 180		
Db	121	GATCCATCCCTTCATGATCCAGCATCTTGATAGAGCAACAGCAATAGCAATGTGGCTCTGCAAGATT 180		
QY	181	GTAATATTAGTCCACCGCCCTCAGGAGAAACAAATAGCAATGTGGCTCTGCAAGATT 240		
Db	181	GTAATATTAGTCCACCGCCCTCAGGAGAAACAAATAGCAATGTGGCTCTGCAAGATT 240		
QY	241	CTGAACAGCAGTCTCTCCCTCAGGAGCACTGATCTTAAATGATTTTCTTATAGGCG 300		
Db	241	CTGAACAGCAGTCTCTCCCTCAGGAGCACTGATCTTAAATGATTTTCTTATAGGCG 300		
QY	301	ACCGAGCCAGAGGCTTTTATCTGCAAGAGGAGACAGTCTCCAGCGGCTGCTGCTCAG 360		
Db	301	ACCGAGCCAGAGGCTTTTATCTGCAAGAGGAGACAGTCTCCAGCGGCTGCTGCTCAG 360		

QY 361 CTGATTCTAGGAAAGCGCTGGCTGAAGAGGATGTCATCAGAGGCGCTGGATTCTGGATGCG 420
Db 361 CTGATTCTAGGAAAGCGCTGGCTGAAGAGGATGTCATCAGAGGCGCTGGATTCTGGATGCG 420
QY 421 ATCCCTGAGAGCGGTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGACAC 480
Db 421 ATCCCTGAGAGCGGTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGACAC 480
QY 481 GTCAATTGTGTGAGTCTCAGACACCGTCTCTGATCGAGAGAACTTGGGGAGAGAAATC 540
Db 481 GTCAATTGTGTGAGTCTCAGACACCGTCTCTGATCGAGAGAACTTGGGGAGAGAAATC 540
QY 541 GACCTCTAACTGAGAGATTATCACACCACTTTGACTGGCCACCCGAAATCTGAAATC 600
Db 541 GACCTCTAACTGAGAGATTATCACACCACTTTGACTGGCCACCCGAAATCTGAAATC 600
QY 601 CAGAACCGTCTCATGTGTCAGAGAGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGCTG 660
Db 601 CAGAACCGTCTCATGTGTCAGAGAGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGCTG 660
QY 661 GAGTATCATAGAAACATCGTCAGGGTCAATCCCTTACCCCAAAATCTCAAGTCATC 720
Db 661 GAGTATCATAGAAACATCGTCAGGGTCAATCCCTTACCCCAAAATCTCAAGTCATC 720
QY 721 AGTGTGACCAAGCCATGTGAGAGCTCTTACCAAGGCTCTGACCTATGTCCAAAGCAAC 780
Db 721 AGTGTGACCAAGCCATGTGAGAGCTCTTACCAAGGCTCTGACCTATGTCCAAAGCAAC 780
QY 781 CATCGTACTTAATGCCCGCTTACCCCGAGGGTGTCTGCTCGGGCTGTGGGAGTGGG 840
Db 781 CATCGTACTTAATGCCCGCTTACCCCGAGGGTGTCTGCTCGGGCTGTGGGAGTGGG 840
QY 841 AAAAGTGTGAGGCGCGCTCTGCGCCAGAAATACAGGCTGTGCAATGTCTGTGTGGG 900
Db 841 AAAAGTGTGAGGCGCGCTCTGCGCCAGAAATACAGGCTGTGCAATGTCTGTGTGGG 900
QY 901 CAACTGCTGAAAGAGGCTGTGAGAGGACCAAGTTTGGCGAGCTCATCCAGCCCTTC 960
Db 901 CAACTGCTGAAAGAGGCTGTGAGAGGACCAAGTTTGGCGAGCTCATCCAGCCCTTC 960
QY 961 TTTGAAAGAGGATGGAGTCTCTGACAGCTCTCATGAAGTGTCTGAGCAGGCGCTG 1020
Db 961 TTTGAAAGAGGATGGAGTCTCTGACAGCTCTCATGAAGTGTCTGAGCAGGCGCTG 1020
QY 1021 GACCAAGAGGATGGAGTCTCTGACAGCTCTCATGAAGTGTCTGAGCAGGCGCTG 1080
Db 1021 GACCAAGAGGATGGAGTCTCTGACAGCTCTCATGAAGTGTCTGAGCAGGCGCTG 1080
QY 1081 CAGGCAACCTGTGTAACCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGTG 1140
Db 1081 CAGGCAACCTGTGTAACCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGTG 1140
QY 1141 CCAATTGATTCATGAGAGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
Db 1141 CCAATTGATTCATGAGAGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
QY 1201 AGGTACCACTCATGTAAGAGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1260
Db 1201 AGGTACCACTCATGTAAGAGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1260
QY 1261 AACCCAAAGAGTGTGAGAGAGGCTCAAGTGAATGAGCTGTCTTACAGGAATCA 1320
Db 1261 AACCCAAAGAGTGTGAGAGAGGCTCAAGTGAATGAGCTGTCTTACAGGAATCA 1320
QY 1321 GCTGACTTGGAGAGTGTGATGGTGGGCTCAATCCCTCAATGGGACCAAGACCCATAC 1380
Db 1321 GCTGACTTGGAGAGTGTGATGGTGGGCTCAATCCCTCAATGGGACCAAGACCCATAC 1380
QY 1381 ACAGTCTTCGAATACATCGAGAGTGGGATCATTAATCCCTGCGCCAGAAATCCCTCA 1440
Db 1381 ACAGTCTTCGAATACATCGAGAGTGGGATCATTAATCCCTGCGCCAGAAATCCCTCA 1440

RESULT 2
US-10-141-634-3
; Sequence 3, Application US/10141634
; Patent No. 6734010
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6734010el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 285
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-141-634-3
Query Match 19.8%; Score 285; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 9.1e-74;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1156 ATGGAGCGGCTGACTCTCAGAGAAATGATCCAGTCACTGGGAAAGGTACCACTCATG 1215
Db 1 ATGGAGCGGCTGACTCTCAGAGAAATGATCCAGTCACTGGGAAAGGTACCACTCATG 60
QY 1216 TACAGACCACTCCACCATCGAGATCCAGGCTGGCTCTCCAGAAACCCAAAGGATGCT 1275
Db 61 TACAGACCACTCCACCATCGAGATCCAGGCTGGCTCTCCAGAAACCCAAAGGATGCT 120
QY 1276 GAAGAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1335
Db 121 GAAGAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
QY 1336 TTGTATGGTGGGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1395
Db 181 TTGTATGGTGGGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 240
QY 1396 ATCGAGAGTGGGATCAATTAATCCCTGCGCCCAAGAAATCCCTGA 1440
Db 241 ATCGAGAGTGGGATCAATTAATCCCTGCGCCCAAGAAATCCCTGA 285
RESULT 3
US-09-513-999C-3495
; Sequence 3495, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3495
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 67..264


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FEATURE:
NAME/KEY: misc_feature
LOCATION: 12
OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 35
OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 55
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 188
OTHER INFORMATION: w=a or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 202
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 217
OTHER INFORMATION: y=c or t
FEATURE:
LOCATION: 222
OTHER INFORMATION: m=a or c
FEATURE:
LOCATION: 228
OTHER INFORMATION: s=g or c
FEATURE:
LOCATION: 41
OTHER INFORMATION: Xaa=Ile or Asn
FEATURE:
LOCATION: 46
OTHER INFORMATION: Xaa=Leu or Val
FEATURE:
LOCATION: 51
OTHER INFORMATION: Xaa=Pro or Ser
FEATURE:
LOCATION: 52
OTHER INFORMATION: Xaa=Asp or Glu
US-09-513-999C-3495

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Query Match
Best Local Similarity 7.7%; Score 111; DB 4; Length 264;
Matches 154; Conservative 0; Mismatches 5; Indels 36; Gaps 1;

QY 1 ATGAGCGCCACTATGCGCCGACCGTATCCCGCCGAGATGCCCGAGATGCCCGAGAGAG 60
DB 67 ATGAGCGCCACTATGCGCCGACCGTATCCCGCCGAGATGCCCGAGAGAGAG 126
QY 61 AACCATCTTCAGTTGATG-----CAG 84
DB 127 AACCATCTTCAGTTGATGAGTATTAAACCATCTGGGTGTCTGCCCTGCACCCACAG 186
QY 85 AACATGCTGAGCAACTCTGATCCACAGCCGAGATCCCATCCCTTCATCATCCAG 144
DB 187 AWCATGCTGGAGCAASTCTGATCCACAGYCCGAGATCCCATCCCTTCATCATCCAG 246
QY 145 CACTTCATAGAGAC 159
DB 247 CACTTCATAGAGAC 261

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RESULT 4
US-09-252-991A-4328/c

```

; Sequence 4328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4328
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4328

Query Match
Best Local Similarity 4.6%; Score 66.4; DB 4; Length 747;
Matches 206; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

QY 807 GAGGGTGTCTGCTCGGGCTGTGGCGAGTGGGAAAGTCTGCAGCGCCCTCTTGGC 866
DB 730 GCGTGTGATTCTGCTCGGGGACCCGCGTGGCGGAAAGGACCCAGGACGGTTTATCAC 671
QY 867 CCAGAAATACAGGCTTGTCATGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGA 926
DB 670 CGAGAAGTTGCGCATTCGCGATCTCCACCGCGCAGATCTGCGCGCGCAGTCAAGGC 611
QY 927 TAGSACCAGTTTGGCGAGCTCATCCAGCCCTCTTTTGAAGAGGAGATGGCAGTTTCCTGA 986
DB 610 CGGCAGCCCGCTCGGCCAGAGGTGAAGGCGTGTGACAGCGCGCGCTGTATCCGA 551
QY 987 CAGCCTCTCATGAAGAGTGTGAGCGAGCGCTGGACAGCAGGAGTGCATCCAGAAAGG 1046
DB 550 CGACATCATCATCGCCCTGTATCAAGGAACGCATCCAGAGGCGGATTTGGCCAG--GG 494
QY 1047 CTGGGTGTACACAGCGCTCCCGGGACCTCGACAGGACACACCTGCTGAACCGCTGGG 1106
DB 493 CTTCCTGTTGAGCGCTTCCCGCGACCATCCCGCAGGCGGAGCGCTGAAGGACGCGCG 434
QY 1107 CTACATCCCAACAGGCTGTTTTCTTGAATGTGCATTTGATTCATCATGAGCGGCT 1166
DB 433 TGTGACCATCGACACGCTGCTGAGATTCGCGCTCGACGACGAGGAGATCGTGTGCGGTAT 374
QY 1167 GACTCTGAGAAATTTGATCCAGTCTGAGTGGGAAAGGTACACCTCATGTACAAGCCACC 1226
DB 373 CGCCGCTGCTGCGGTGATCCGCGCTCGGCGCGGTGTATACACACCGAGCAGACCGCCG 314

RESULT 5
US-09-252-991A-4185/c
; Sequence 4185, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4185
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

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Mon Mar 21 09:11:06 2005

US-09-252-991A-4185

Query Match 4.6%; Score 66.4; DB 4; Length 792;
 Best Local Similarity 49.0%; Pred. No. 4.1e-09;
 Matches 206; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
 QY 807 GAGGCTCTGCTGCTGGGCTGTGGCAGTGGGAAAGTCTGCAGCGCGCTCTCTGGC 866
 DB 492 GCGTGTGATTCTGCTCGGGGACCCCGGTGCGGCAAGAGGACCCAGGACGGTTTATCAC 433
 QY 867 CCAGAAATACAGGCTTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGA 926
 DB 432 CGAGAGTTCCGATTCGGCAGATCTCCACGGGACATGCTCGCGCGCAGTCAAGGC 373
 QY 927 TAGGACCAAGTTTGGCAGCTATCCAGCCCTTCTTTGAAAGAGAGATGGCAGTTCTTGA 986
 DB 372 CGGACGCGCTCGGCGCAGCAGGTGAAAGGCGTGTGAGCAGCGCGGCTGTGTATCCGA 313
 QY 987 CAGCTCTCTATGAGTGTGAGCCAGCGCTGAGCAGCAGCAGTGTGATCCAGAAAGG 1046
 DB 312 CGACATCATCATCGCCCTGATCAGAGAACGATCACCAGGCGGATTTGGCCCAAG---GG 256
 QY 1047 CTGGGTGCTACACGCGCTCCCGCGGACCTCGACGAGCAGCAGTGTGTAACCGCTGGG 1106
 DB 255 CTTCCTGTTTCGAGGCTTCCCGCGGACCATCCCGCAGGCGGAAAGCGCTGAAGACGCGG 196
 QY 1107 CTACATCCCAACAGGCTGTTTCTGTAATGTGCCATTTGATTCATCATGAGCGGCT 1166
 DB 195 TGTGACCATCGACACCGTGTGAGATCGCCGTGACGACGAGAGATCGTGTGCGGTAT 136
 QY 1167 GACTCTGAGAGAAATGTATCCAGTCACTGCGGAAAGGTACACCTCATGTATCAAGCCACC 1226
 DB 135 CGCCGCTGCTCGCTGCATCCGGCTCCGGCGCGGTGTATCCACACCGAGCAGCACCGCGC 76

RESULT 6

US-09-252-991A-4526
 ; Sequence 4526, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 4526
 ; LENGTH: 849
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-4526

Query Match 4.6%; Score 66.4; DB 4; Length 849;
 Best Local Similarity 49.0%; Pred. No. 4.2e-09;
 Matches 206; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
 QY 807 GAGGCTCTGCTGCTGGGCTGTGGCAGTGGGAAAGTCTGCAGCGCGCTCTCTGGC 866
 DB 204 GCGTGTGATTCTGCTCGGGGACCCCGGTGCGGCAAGAGCACCAGGACGGTTTATCAC 263
 QY 867 CCAGAAATACAGGCTTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGA 926
 DB 264 CGAGAGTTCCGATTCGGCAGATCTCCACCGCGCAGATGCTCGCGCGCAGTCAAGGC 323
 QY 927 TAGGACCAAGTTTGGCAGCTATCCAGCCCTTCTTTGAAAGAGAGATGGCAGTTCTTGA 986
 DB 324 CGGACGCGCTCGGCGCAGCAGGTGAAAGGCGTGTGAGCAGCGCGGCTGTGTATCCGA 383

QY 987 CAGCTCTCTATGAAAGTGTGAGCCAGCGCTGTGGACCGAGGACTGTGATCCAGAAAGG 1046
 DB 384 CGACATCATCATCGCCCTGATCAAGAACGCATCACCGAGGCGCGATTTGGCCCAAG---GG 440
 QY 1047 CTGGGTGCTACAGGCGTCCCGGAGCTTCGACACGAGGACACCTCTCTGAACCGCTGGG 1106
 DB 441 CTTCCTGTTTCGACGCTTCCCGGGACCATCCCGCAGGCGGAGCGCTGAAGACGCCGG 500
 QY 1107 CTACAAATCCCAACAGGCTGTTTCTGTAATGTGCCATTTGATTCATCATGAGCGGCT 1166
 DB 501 TGTGACCATCGACACCGTGTGAGATCGCCGTGACGACGAGAGATCGTGTGCGGTAT 560
 QY 1167 GACTCTGAGAGAAATGTATCCAGTCACTGCGGAAAGGTACACCTCATGTATCAAGCCACC 1226
 DB 561 CGCCGCTGCTCGCTGCATCCGGCTCCGGCGCGGTGTATCCACACCGAGCAGCACCGCGC 620

RESULT 7

US-09-252-991A-4423
 ; Sequence 4423, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 4423
 ; LENGTH: 1002
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-4423

Query Match 4.6%; Score 66.4; DB 4; Length 1002;
 Best Local Similarity 49.0%; Pred. No. 4.7e-09;
 Matches 206; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
 QY 807 GAGGCTCTGCTGCTCGGCGCTGTGGCAGTGGGAAAGTCTGCAGGCGCGCTCTCTGGC 866
 DB 163 GCGTGTGATTCTGCTCGGGGACCCCGGTGCGGCAAGGACCCAGGACCGGTTTATCAC 222
 QY 867 CCAGAAATACAGGCTTGTCAATGTCTGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCAGA 926
 DB 223 CGAGAGTTCCGCAATTCGGCAGATCTCCACCGCGGACATGCTGCGCGCGCAGTCAAGGC 282
 QY 927 TAGGACCAAGTTTGGGCGAGCTCATCCAGCCCTTCTTTGAAAGAGAGATGGCAGTTCTTGA 986
 DB 283 CGGACGCGCTCGGCGCAGCAGGTGAAAGGCGGTGTATGAGCAGCGCGGCTGTGTATCCGA 342
 QY 987 CAGCTCTCTATGAAAGTGTGAGCGCGCTGTGGACCGAGCAGTGTGATCCAGAAAGG 1046
 DB 343 CGACATCATCATCGCCCTGATCAAGAACGCATCACCGAGGCGGATTTGGCCCAAG---GG 399
 QY 1047 CTGGGTGCTACAGCGCTCCCGGAGCTTCGACACGAGGACACCTGTGTAACCGCTGGG 1106
 DB 400 CTTCCTGTTTCGACGCTTCCCGGGACCATCCCGCAGGCGGAGCGCTGAAGACGCCGG 459
 QY 1107 CTACAAATCCCAACAGGCTGTTTCTGTAATGTGCCATTTGATTCATCATGAGCGGCT 1166
 DB 460 TGTGACCATCGACACCGTGTGAGATCGCCGTGACGACGAGAGATCGTGTGCGGTAT 519
 QY 1167 GACTCTGAGAGAAATGTATCCAGTCACTGCGGAAAGGTACACCTCATGTATCAAGCCACC 1226
 DB 520 CGCCGCTGCTCGCTGCATCCGGCTCCGGCGCGGTGTATCCACACCGAGCAGCACCGCGC 579

RESULT 8

US-09-489-039A-5541
; Sequence 5541, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIORITY FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5541
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5541

Query Match 4.4%; Score 63.2; DB 4; Length 678;
Best Local Similarity 48.8%; Pred. No. 3.3e-08;
Matches 201; Conservative 0; Mismatches 208; Indels 3; Gaps 1;
QY 815 TGCTCTCGGCGCTGTGGCAGTGGGAAAGTCTGCAGCGCGCTCTGCGCCAGAAAT 874
DB 44 TTCTCTTTGGCGCTCCGGCGCGGGTAAAGAACTCAGGCTCAGTTTCATCATGAGAAAT 103
QY 875 ACAGGCTTGTCAATGCTGTGTGGCAACTCTGTAAGAGGCTGTGGCAGATAGGACCA 934
DB 104 ACGTATTCGCAAAATCTCCACCGGATATGTCGCGCGCGGTAAATTCGGCTCTG 163
QY 935 CTTTGGGAGCTCATCCAGCCCTCTTTGAAAGAGATGGCAGTTCTGTGACAGCTCC 994
DB 164 AGCTCGGTAAGCAGCGAAAGACATATGAGCAGGCAAGCTGGTGACGATGAGCTGG 223
QY 995 TCATGAAGTGTGTGAGCAGCGCTGACACGAGGACTCATCCAGAAAGCTGGTGCC 1054
DB 224 TCATCGCGTGGTGAAGAGCGTATCGCCCGAGATTG---CCGTACGCGCTTCCTGC 280
QY 1055 TACACGCGCTCCCGCGGACCTCGACAGGACACTGCTGAACCGCTGGGCTACAATC 1114
DB 281 TGGACGCTTCCCGCGGACATTCGCGAGGCTGACGCATGAAGAGGCGGCAATACCG 340
QY 1115 CCAACAGGCTTTTTCCTGAAATGCAATTTGATCCATCATGGAGCGGCTGACTGTA 1174
DB 341 TTGATTCAGTGTGGAAATTCGACGTGCCGAGCAACTGATCGTCGACCGCATCGTTGCC 400
QY 1175 GAAGAAATGATCAGTCACTGGGGAAGGTACCACTCATGTATCAAGCCACC 1226
DB 401 GTCGCGTCCACGCGGCATCCGCTCGCGTATACCAATCAATTCGCGCC 452

RESULT 9
US-08-829-027-2
; Sequence 2, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,027
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 2122022
US-08-829-027-2
Query Match 3.9%; Score 56.8; DB 2; Length 854;
Best Local Similarity 48.9%; Pred. No. 2.9e-06;
Matches 216; Conservative 0; Mismatches 217; Indels 9; Gaps 2;
QY 805 CCGAGGGTGTGCTGTGCGGCTGTGGGCTGTGGGCAAGTGTGAGGCGGCTGTGCA 864
DB 72 CTGGAGCGGTGATCATGCGGGGCGCGGCTCGGGCAAGGCGCACCGTGTGTCGGCATC 131
QY 865 GCCAGAAATACAGGCTTGTCAATGTCTGTGTGGGCAACTGTGAAAGAGGCTGTGSCA 924
DB 132 ACTACACACTTCGAGCTGAAGCAGCTCTCCAGCGGGGACTCTCTCGGGCAACATGCTG 191
QY 925 GATAGACCACTTTGGGAGCTCATCCAGCCCTCTTTGAAAGAGGATGGCAGTTCTCT 984
DB 192 CGGGGACAGAAATTTGGCGTGTAGCCAAGCTTTCAITGACCAAGGAACTCATCCCA 251
QY 985 GACAGCTCTCATGAAGTGTCTGAGCCGCTCGACCGGCTCGACAGGAGCTGATCAAGAA 1044
DB 252 GATGATGTCATGACTCGGCTG-----GCCCTTCATGAGCTGAAAAATCTCACCAGTAT 305
QY 1045 GGTGGTGTCTACAGGCTCCCGGGAGCTTCGACAGGACACCTGCTGTAACCGGCTG 1104
DB 306 AGTGGCTGTGGATGTTTTTCCAAGGACACTTCCACAGGCAAGAGCCCTAGATAG--A 362
QY 1105 GGTCAATCCCAACAGGCTGTTTTTCTGAATGTGCCATTTGATTCATCATGGAGCGG 1164
DB 363 GCTTATCAGATCGACACAGTGATTAACTGAAATGTGCCCTTTGAGTTCATTAAACAGC 422
QY 1165 CTGACTCTGAGAAGATTGATCCAGTCACTCGGGGAAGGTACCACTCATGTACAGCCA 1224
DB 423 CTTACTGCTGCTGATTCATCCGCGAGTGGCCGAGTCTATAACATTAATTAACACCT 482
QY 1225 CTTCCCAACATGGAGTCCAGG 1246
DB 483 CCAAAACTGTGGGCATTGATG 504

RESULT 10
US-09-225-366-2
; Sequence 2, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

us-10-798-773-1.rn1

Mon Mar 21 09:11:06 2005

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,366

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/829,027

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PP-0256 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 854 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: Consensus

CLONE: 2122022

US-09-225-366-2

Query Match 3.9%; Score 56.8; DB 3; Length 854;

Best Local Similarity 48.9%; Pred. No. 2.9e-06;

Matches 216; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

QY	805	CCGAGGTCCTGCTGCTGGGCTGTGGCGAGTGGGAAAGTCTGCAGGCGGCTCTG	864
Db	72	CTGCGAGCGTGTATGATGCGGGGCCCGCGGCTCGGCAAGGGACCGTGTCTCGCGATC	131
QY	865	GCCAGAAATACAGGCTTGTCAATGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA	924
Db	132	ACTACACATTCAGCTGAGCTGAGCACCTCTCCAGCGGGACCTGCTCCGGGCAACATGCTG	191
QY	925	GATAGGACCAAGCTTTGGCGAGCTCATCCAGCCCTTCTTTGAAAGGAGATGGCAGTTCCT	984
Db	192	CGGGGCACAGAAATTTGGCGTGTAGCCAAAGGCTTTTCATTTGACCAAGGAAACTCATCCCA	251
QY	985	GACAGCTCTCATGAGGTGCTGAGCCAGCGCTGGACGACGAGCTGTCATCCAGAAA	1044
Db	252	GATGATGTCTGATGACTCGGCTG-----GCCCTTCATGAGCTGAAATCTCACCCAGTAT	305
QY	1045	GGCTGGGTGTCTACACGCGCTCCGCGGAGCCTCGACGACGACACCTGCTGACCGCTG	1104
Db	306	AGTGTGCTGTGGATGGTTTTCACAGGACACTTCCACAGGCAAGAGCCCTAGATAG--A	362
QY	1105	GGCTACATCCCAACAGGCTGTTTTCCTGATGTCGCAATTTGATTCATCATGAGCGG	1164
Db	363	GCTTATCAGATCAGACAGGATTAACCTGATGTCCTTTGAGGTCTATTAACACGC	422
QY	1165	CTGACTCTGAGAGAAATTTGATCCAGTCACTGCGGAAAGTACCACTCATGTACAGCCA	1224
Db	423	CTTACTGCTGCTGGATTCATCCCGCAGTGGCGGAGTCTATAACATTCGATTCACCT	482
QY	1225	CTTCCCAACATGAGGATCCAGG	1246
Db	483	CCCAAACTGTGGCATTGATG	504

RESULT 11

US-09-149-476-68
; Sequence 68, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
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; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11

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EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
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EARLIER APPLICATION NUMBER: 60/056,889
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
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EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
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EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 3.9%; Score 56.8; DB 3; Length 1751;

Best Local Similarity 48.9%; Pred. No. 4,3e-06;

Matches 216; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

QY 805 CCGAGGTGCTGCTGCTCGGGCTGTGGGAGTGGGAAAAGTGTGCGAGCCGCCCTCTG 864
Db 116 CTGCGAGCGGTGATCATGGGGGCCCCCGGGCTCGGGCAAGGGCCACCGTGTGTCGGGCATC 175
QY 865 GCCCAGAAATACAGGCTTGTCAATGCTGTGGGCAACTGTCTGAAAGAGGCTGTGGCA 924
Db 176 ACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGACCTGCTCCGGGACCAACATGTC 235
QY 925 GATAGGACACAGTTCGGCGAGCTCATCCAGGCCCTTCTTTCAAAAGAGATGCACTTCT 984
Db 236 CGGGGCACAGAAATTGGCGTGTAGCAAGGCTTTCATTGACCAAGGAACTCATCCCA 295

Mon Mar 21 09:11:06 2005

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5838
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-5838

Query Match 2.9%; Score 41.8; DB 4; Length 2237;
Best Local Similarity 44.7%; Pred. No. 0.13; 202; Indels 0; Gaps 0;
Matches 163; Conservative 0; Mismatches 0; Gaps 0;
QY 802 ACCCGAGGGTGTCTGCTCGGGCTGTGGGCGAGTGGGAAAAGTCTGCGAGGCGCCCTC 861
DB 56 ACCAAGATCATCTTTGTGGTGGGCTGCTCAGGGAAGGCGACCCAGTGTGAGAAG 115
QY 862 CTGGCCCCAAGAAATACAGGCTTGTCAATGTCTGTGTGGCAACTGCTGAAAAGGCTGTG 921
DB 116 ATCGTGCAAGATATGGCTACACCCACTCTCCACCGGGGACCTCTCGCGTCCGAGTTC 175
QY 922 GCAGATAGGACCACTTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAGTT 981
DB 176 AGCTCAGGCTGGCCAGGGGCAAGAGCTGTGCGAATCATGGAGAGGGGCGAGTGT 235
QY 982 CTGACAGCTCTCATGAAGGTGTGAGCCAGGCGCTGACCGACGAGGACTGTCATCCAG 1041
DB 236 CCACTGGAGACAGTGTGGACATGCTCCGGATGCTGCTGGGCGGATGCTGCTGCTGCTG 295
QY 1042 AAAGCTGGTGTCTACACGGGCTCCCGGGGACCTTCGACCGAGGCGACACCTCTGTAACCGC 1101
DB 296 AAAGGCTTCTGATGATGGCTACCCGCGGGAGGTGCGAGGAAGAGAGTTTGAGCGA 355
QY 1102 CTGGGCTACAAATCCCAACAGGTTTTCCTGATGTGCCATTTTCATTCATCATGAG 1161
DB 356 CGGATTGGACAGCCCACTGCTGTGTATGTGGACGCGAGGCGCTGAGACCATGACCCAG 415
QY 1162 CGGCT 1166
DB 416 CGGCT 420

RESULT 14
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:

QY 985 GACAGCTCTCTCATGAAGTGTGTAGCCAGCGCTGGACACGAGCTGCAATCCAGAAA 1044
DB 296 GATGATGTCTAGTCTGGCTG-----GCCCTCATGAGCTGAAAATCTCACCCAGTAT 349
QY 1045 GGCTGGGTGTCTACACGGCGTCCCGGGAGCTTGGACGAGCACCTGCTGAACCGCTG 1104
DB 350 AGCTGGCTGTGTGATGTTTCCAAAGGACACTTCCACGGCGAAGCCCTAGATAG---A 406
QY 1105 GGCTACATCCCAACAGGGTGTTCCTCAATGTGCCATTTGATTCATCATGAGCGG 1164
DB 407 GCTTATCAGATCCACAGATTAACCTGAATGTGCCCTTTGAGGTCAATTAACAGCG 466
QY 1165 CTGACTCTGAGAAGATTTGATCAGTCACTGGGGAAGGTACACCTCATGTACAGCCA 1224
DB 467 CTACTCTGCTGATTCATCCGCGAGTGGCGAGTCTATAACATTTGAATTTCAACCT 526
QY 1225 CTTCCACCATGGAGATCCAGG 1246
DB 527 CCCAAACTGTGGCATTTGATG 548

RESULT 12
US-09-489-039A-3207
; Sequence 3207, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3207
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3207

Query Match 2.9%; Score 41.8; DB 4; Length 1866;
Best Local Similarity 46.9%; Pred. No. 0.12;
Matches 130; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
QY 998 TGAAGTGTGAGCCAGCGCTGGACGAGCTGCAATCCAGAAAGGCTGGGTGTCTAC 1057
DB 1076 TGAAGTGGCGGCTGTGCGATGCGCATAGTCAGTACGGATCTCTGTGGGAGCTGCGG 1135
QY 1058 ACGGCTCCCGGGACCTCGACGAGGCACTCTGTGAACCGCTGGGCTACATCCCA 1117
DB 1136 TTGGCGCCATCTCAGCCAGCATCAGCAGCTGTGGATACCTGTGGAACTGGA 1195
QY 1118 ACAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGAGCGGCTGACTCTGAGAA 1177
DB 1196 CCAGCAGCTTGGGCTGGACCGCATCAGGAGAGCAGAGCTGATCGTATGGAAG 1255
QY 1178 GAATTGATCAGTCACTGGGGAAGGTACCACTCATGTACAGGCACTCCACATGG 1237
DB 1256 ACGGGCCATATGCGCGCGAGCTGACGACTCCATCGCCAGTCCGCTATCTGTATGA 1315
QY 1238 AGATCCAGGTGCGCTCTCGAGACCCAAAGATGC 1274
DB 1316 AGATGCAAGTGTGTCTGAGATGCAAGGCGACGC 1352

RESULT 13
US-09-949-016-5838
; Sequence 5838, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.8%; Score 40.4; DB 3; Length 4403765;
Best Local Similarity 48.7%; Pred. No. 25;
Matches 110; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 807 GAGGGTCTGCTGCTCGGGCTGTGGGCACTGTGGGAAAGTCTGCAGGCGCCCTCTCTGGC 866
DB 828301 GAGAGTTTGTGCTGGGACCGCCGGGGGCGGCAAGGAGCGAGCGGTGAAGCTGGC 828360
QY 867 CCAGAAATACAGGCTTGTCTATGCTGTGGGCACTGTCTGAAAGAGGCTGTGGCAGA 926
DB 828361 CGAGAAGCTTCGGATCCCGCAGATCTCCACCGCGCAACTCTTCCGGCGCAACATCGAAGA 828420
QY 927 TAGGACCAAGTTTGGGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAGTCTCTGA 986
DB 828421 GGGCACCAGCTCGGCTGGAAGCAACGCTACTTGGATCGCGTACTTGGTGGCGTC 828480
QY 987 CAGCCTCTCATGAAGTGTGAGCCAGCGCTGACCAGCAGGAC 1032
DB 828481 CGACTTGACCAATGAATCTGTCGACGACCGGCTGAACAATCCGAC 828526

RESULT 15

US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.8%; Score 40.4; DB 3; Length 4411529;
Best Local Similarity 48.7%; Pred. No. 25;
Matches 110; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
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DB 826122 GAGAGTTTGTGCTGGGACCGCCGGGGGCGGCAAGGAGCGAGCGGTGAAGCTGGC 826181
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DB 826182 CGAGAAGCTTCGGGATCCCGCAGATCTCCACCGCGCAACTCTTCCGGCGCAACATCGAAGA 826241
QY 927 TAGGACCAAGTTTGGGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAGTCTCTGA 986
DB 826242 GGGCACCAGCTCGGCTGGAAGCAACGCTACTTGGATGCGGTGACTTGGTGGCGTC 826301
QY 987 CAGCCTCTCATGAAGTGTGAGCCAGCGCTGACCAGCAGGAC 1032
DB 826302 CGACTTGACCAATGAATCTGTCGACGACCGGCTGAACAATCCGAC 826347

Search completed: March 19, 2005, 23:53:51
Job time : 293 secs

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 20:29:39 ; Search time 4381 Seconds
 (without alignments)
 12511.424 Million cell updates/sec

Title: US-10-798-773-1

Perfect score: 1440

Sequence: 1 atggcagccactatcgccgc.....tgcccaagaataccctga 1440

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_ga81.*

9: gb_ga82.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1025.4	71.2	2567	3	BC037402 Homo sapi
2	912.8	63.4	1559	3	AK004439 Mus muscu
3	911.8	63.3	1094	5	BM920443 AGENCOURT
4	805.6	55.9	886	6	CD151464 AGENCOURT
5	783.2	54.4	890	4	BI819382 AGENCOURT
6	743.6	51.6	1130	5	BM926674 AGENCOURT
7	723.2	50.2	827	4	BI829572 AGENCOURT
8	703	48.8	710	4	BI767614 AGENCOURT
9	670	46.5	670	4	BI828586 AGENCOURT
10	656	45.6	657	7	CV030269 AGENCOURT
11	591	41.0	721	5	BU617945 AGENCOURT
12	547	38.0	685	5	BQ016312 AGENCOURT
13	518.4	36.0	996	6	BY704667 AGENCOURT
14	514.2	35.7	550	5	BP368808 AGENCOURT
15	513.8	35.7	583	2	BP347783 AGENCOURT
16	463	32.2	463	2	AW069362 AGENCOURT
17	463	32.2	608	5	BU683145 AGENCOURT
18	448	31.1	705	1	AI591934 AGENCOURT
19	441.6	30.7	716	7	CK476676 AGENCOURT
20	422.4	29.3	934	5	BQ942240 AGENCOURT
21	417.6	29.0	794	7	CK594922 AGENCOURT
22	413.8	28.7	857	7	CK653506 AGENCOURT
23	408.6	28.4	789	7	CK470906 AGENCOURT
24	403	28.0	845	7	CK468902 AGENCOURT

25	387.6	26.9	835	7	CK595309
26	386.2	26.8	534	1	AI826091
27	386	26.8	622	2	BF469787
28	383.4	26.6	608	7	CF360290
29	377.8	26.2	611	6	CB274665
30	362	25.1	838	5	BU938366
31	361	25.1	488	5	BM983192
32	350.8	24.4	715	7	CN834879
33	348.6	24.2	601	7	CO602574
34	343	23.8	453	1	AI361512
35	341.2	23.7	398	5	BM991015
36	323.2	22.4	493	2	AW663881
37	322.4	22.4	602	1	AB046366
38	322	22.4	436	1	AA580077
39	322	22.4	444	1	AI362274
40	322	22.4	464	1	AI359456
41	322	22.4	500	5	EX100680
42	322	22.4	552	2	AW974034
43	320.4	22.2	850	5	BU954715
44	296.6	20.6	730	7	CK653394
45	290	20.1	826	5	EX742486

ALIGNMENTS

RESULT 1
 BC037402
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BC037402 2567 bp mRNA linear HTC 25-MAR-2004
 Homo sapiens chromosome 9 open reading frame 98, mRNA (cDNA clone IMAGE5163904), with apparent retained intron.
 BC037402 GI:23336941
 HTC.
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2567)

REFERENCE
 AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stachton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullay, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Scherch, A., Schein, J.E., Jones, S.O. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

JOURNAL
 PUBLISHED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

REMARK
 COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapb-r@mail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.

cdDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgobcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulse
Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanav
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 52 Row: i Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomesScan gene prediction
analysis, and the following problem: retained intron.

FEATURES Location/Qualifiers

Source

```

1. 2567
Location/Qualifiers
  organism="Homo sapiens"
  mol_type="mRNA"
  db_xref="taxon:9606"
  clone="IMAGE:5163904"
  tissue_type="Brain, adult"
  clone_lib="NIH_MGC_119"
  lab_host="DH10B"
  notes="Vector: pCMV-SPORT6"

```

ORIGIN

Query Match	71.2%;	Score 1025.4;	DB 3;	Length 2567;
Best Local Similarity	78.5%;	Pred. No. 1.5e-262;	Indels 393;	Gaps 2;
Matches 1439;	Conservative	0;	Mismatches 1;	
1	ATGACGCGCCACTATCGCCCCCGCACCGTATCCCCCCCGAGATGCCCCAGTAGTACGGGGAGGAG	60		
523	ATGGACGCCCACTATCGCCCCCGCACCGTATCCCCCCCGAGATGCCCCAGTAGTACGGGGAGGAG	582		
61	AACACACATCTTTCGAGTTGATGCAGAACATGCTGGAGCAATCTCTGTATCCACACAGCCCGGAA	120		
583	AACACACATCTTTCGAGTTGATGCAGAACATGCTGGAGCAATCTCTGTATCCACACAGCCCGGAA	642		
121	GATCCCATCCCTTTCATGATCCAGCACTTTGCANATAGACAACAGCAAT	168		
643	GATCCCATCCCTTTCATGATCCAGCACTTTGCATAGAGCAACAGCAATGCTGTTTGAAG	702		
169	-----	168		
703	GAGCTACAGTGCACCAGTTGAATTAGTGCTTTGGTACAGCTGAGGACAGAGCCCCAGAGAT	762		
169	-----GTGCGCCAGGATTCGTATATATTAGTCTCCACCCCGC	200		
763	GCCCTGTGTGGAGTTTCAGAAAGCCCAAGTGGCCAGGATTTGTAATATTAGTCTCACCCCGC	822		
201	CTCAGGAGAAACAAACATAGCAATGTGGCTCTGCAAAACATCTGAACAGCAGTCTCTCTAC	260		
823	CTCAGGAGAAACAAACATAGCAATGTGGCTCTGCAAAACATCTGAACAGCAGTCTCTCTAC	882		
261	CCTGGAGAACCTGATCTTAATACAGTTTTCCTATACGCCACCGAAAGCCAGAGGCTTTTA	320		
883	CCTGGAGAACCTGATCTTAATACAGTTTTCCTATACGCCACCGAAAGCCAGAGGCTTTTA	942		
321	TCTGCAAGGAGAACAGTTTCCAGCGCGTCTGCTGCTCAGCTGATTCAGGAAACGCTTGGC	380		
943	TCTGCAAGGAGAACAGTTTCCAGCGCGTCTGCTGCTCAGCTGATTCAGGAAACGCTTGGC	1002		
381	TGAGAGGATTTGCATCAAGCAGGCGTGGATTTCTGGATGGCATCCCTTGAGACGCGTGAACA	440		
1003	TGAGAGGATTTGCATCAAGCAGGCGTGGATTTCTGGATGGCATCCCTTGAGACGCGTGAACA	1062		
441	GGCTCTGAGGATTCAGACCTCTGGGATTCACACCCAGACAGCTATTGTCGTGAGTGTCTCC	500		
1063	GGCTCTGAGGATTCAGACCTCTGGGATTCACACCCAGACAGCTATTGTCGTGAGTGTCTCC	1122		

QY	501	AGCAGCGTCTGTATCGAGAGAACTTTCGGGAAGAGATCGACCTCAAACTGGAG-----	556
Db	1123	AGACAGGTCCTGTATCGAGAGAACTTTCGGGAAGAGATCGACCTCAAACTGGAGGTAT	1182
QY	557	-----	556
Db	1183	GGCTACGGCCACCCACCCAGCCCATGGGTTTCAGAGTCCATGTGTATGACAGACCG	1242
QY	557	-----	556
Db	1243	TCTACCATTTCTTGACCTCGCANTTCTGTCTGGGCACCCACAGAGGNACAGGAAGGC	1302
QY	557	-----	556
Db	1303	TGCCACAGGCTGGCTCTGAGCTGGAGACATGGCAAGGACATGGGATACCTGAGACTC	1362
QY	557	-----	556
Db	1363	AGTTTTCTTATCTGTACTTTGAGGTAAAAATACCAACCTAATGGGTGATGGATGGCTGT	1422
QY	557	-----AGATTTATCAC	567
Db	1423	GAAGATGAATGGAGTCTGCAGGTGCCTTATCAGAGTGGCTGGCACAGAATTTATCAC	1482
QY	568	ACCACTTTTGACTGGCCACCCGAAATCTGAAATTCAGAACCGTCTCATGGTGCCAGAGAC	627
Db	1483	ACCACTTTTGACTGGCCACCCGAAATCTGAAATTCAGAACCGTCTCATGGTGGCAGAGAC	1542
QY	628	ATCTCAGAGCTGGAGCGGCTCAGAACTGCTGGAGTATCATAGGAAATCATCTCGAGGTC	687
Db	1543	ATCTCAGAGCTGGAGCGGCTCAGAACTGCTGGAGTATCATAGGACATCTCTCAGGTC	1602
QY	688	ATTCCTCTCTACCCCAAAATCTCAAAGTTCATCAGTGTGACGAGCCATGTGTGACGTC	747
Db	1603	ATTCCTCTCTACCCCAAAATCTCAAAGTTCATCAGTGTGACGAGCCATGTGTGACGTC	1662
QY	748	TTCTACAGGCTTGACCTATGTCCAAAGCAACATCGTACTAAATGCCCGTTTCAACCCG	807
Db	1663	TTCTACAGGCTTGACCTATGTCCAAAGCAACATCGTACTAAATGCCCGTTTCAACCCG	1722
QY	808	AGGCTGTCTGTCTCGGCTGTGGCAGTGGGAAAGTCTGCAGGCCGCTCTCTGGCC	867
Db	1723	AGGCTGTCTGTCTCGGCTGTGGCAGTGGGAAAGTCTGCAGGCCGCTCTCTGGCC	1782
QY	868	CAGAAATACAGGCTGTCAATGTCTGTGTGGCACTGCTGAAAGGCTGTGGCAGAT	927
Db	1783	CAGAAATACAGGCTGTCAATGTCTGTGTGGCACTGCTGAAAGGCTGTGGCAGAT	1842
QY	928	AGGACCGTTTGGGAGCTCATCCAGCCCTCTTTTGAAAGGAGATGGCAGTTCCTGAC	987
Db	1843	AGGACCGTTTGGGAGCTCATCCAGCCCTCTTTTGAAAGGAGATGGCAGTTCCTGAC	1902
QY	988	AGCCTCTCATGAAGGTGCTGAGCCAGCGCTGGAACAGAGACTGCATCCAGAAAGGC	1047
Db	1903	AGCCTCTCATGAAGGTGCTGAGCCAGCGCTGGAACAGAGACTGCATCCAGAAAGGC	1962
QY	1048	TGGGTGCTACAGCGGTCGGGGAGCTCGAACAGGACACCTGCTGAAACCGCTGGGC	1107
Db	1963	TGGGTGCTACAGCGGTCGGGGAGCTCGAACAGGACACCTGCTGAAACCGCTGGGC	2022
QY	1108	TACATATCCCAACAGGGTGTCTTCTGHAATGTCCATTTGATTCATATGAGCGGCTG	1167
Db	2023	TACATATCCCAACAGGGTGTCTTCTGHAATGTCCATTTGATTCATATGAGCGGCTG	2082
QY	1168	ACTCTGAGAAGAAATTGATCTCAGTCACTGGGGAAGGTACCACTCATGTACAGGCCACCT	1227
Db	2083	ACTCTGAGAAGAAATTGATCTCAGTCACTGGGGAAGGTACCACTCATGTACAGGCCACCT	2142
QY	1228	CCACCATCGAGATCCAGGCTCGCTCTCTGACAGAACCCAAAGGATGTGAAGACAGGTC	1287
Db	2143	CCACCATCGAGATCCAGGCTCGCTCTCTGACAGAACCCAAAGGATGTGAAGACAGGTC	2202
QY	1288	AGCTGAAATGGAACCTGTTCTACAGGAACTCAGCTGACTTGGAGCAGTCTGTATGGTCTG	1347

Db 2203 AAGCTGAAATGACCTGTCTTACAGGAATCTCAGCTGACTTGGAGCAGTGTATGGTCTG 2262
 QY 1348 GCCATCACCTCAATGGGGGACAGCCCATACACAGTCTTCGATACATACGAGTGGG 1407
 Db 2263 GCCATCACCTCAATGGGGGACAGCCCATACACAGTCTTCGATACATACGAGTGGG 2322
 QY 1408 ATCATTAATCCCTGCCCAAGAAATCCCTGA 1440
 Db 2323 ATCATTAATCCCTGCCCAAGAAATCCCTGA 2355

RESULT 2

AK004439

LOCUS

DEFINITION

Mus musculus 18-day embryo whole body cDNA, RIKEN full-length
 enriched library, clone:1190002A17 product:similar to CDNA FLJ32704
 FIS, CLONE TEST12000591, WEAKLY SIMILAR TO ADENYLATE KINASE,
 CHLOROPLAST (EC 2.7.4.3) [Homo sapiens], full insert sequence.

ACCESSION

AK004439

VERSION

AK004439.1 GI:12835623

KEYWORDS

HTC; CAP trapper

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Carninci, P. and Hayashizaki, Y.

REFERENCE

1

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

99279253

REFERENCE

2

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

20499374

REFERENCE

3

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

20530913

REFERENCE

4

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

11076861

REFERENCE

5

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

11076861

REFERENCE

6

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

11076861

REFERENCE

7

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tezuka, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN) Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.jp/) for further
 details.

COMMENT

CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in RIKEN
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5' GAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. Second
 strand cDNA was prepared with the primer adapter of sequence [5'
 GAGAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTNN 3']. cDNA was
 cleaved with XhoI and SctI. Cloning sites, 5' end: SctI; 3' end:
 XhoI. Host: SOUR.

FEATURES

source

Location/Qualifiers

1..1559

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

/db_xref="FANTOM DB:1190002A17"

/clone="1190002A17"

/tissue_type="whole body"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="18-day embryo"

misc_feature

29..1467

/note="putative"

similar to CDNA FLJ32704 FIS, CLONE TEST12000591, WEAKLY

SIMILAR TO ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3)

(Homo sapiens) [SPT:Q96MA6, evidence: FASTV, 75.5%ID,

99.7%length, match=1433]"

1544..1549

/note="putative"

1559

/note="putative"

ORIGIN

Query Match 63.4%; Score 912.8; DB 3; Length 1559;

Best Local Similarity 77.6%; Pred No 1.6e-232;

Matches 1117; Conservative 0; Mismatches 322; Indels 1; Gaps 1;

QY 1 ATGGAGCGCATATCGCCCGCAGCTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60

Db 29 ATGGATGCAACACAGCCCTCATCGCATTCGCCGAAATGCCCTAGTACGGGAGAC 88

QY 61 AACCAATCTTCGAGTTGATGCAGAAATCATCTGGAGCAATCTCTGATCCACAGCCGAA 120

Db 89 TACTACATTTTCGAGATGATGCAGAAATCATCTGGAGCAATCTCTGATCCACAGCCGAG 148

QY 121 GATCCCATCCCTTCATGATCCAGCATTTGATGATGATGATGATGATGATGATGATGAT 180

Db 149 GACCCCATCAGTTTCATGATCACTCACTCGCGGAGACATGATATGTCGCAAGTGT 208

QY 181 GTAATATTAGTTCACCCGCTCAGGAAACCAATAGCATATGCTCTGCAAAAT 240

Db 209 GTGATATTAGTTCGCTGCTCAGGAAACCAATAGCATATGCTCTGCAAAAT 268

QY 241 CTGACAGCAGTCTCTCACCCTCGGAGAACCTGATTTTAATAGTCTTCTATACGGCC 300

Db 269 CTAAACAGCAACCTCATCAACCAAGGAGAGCTTACTAGAAAGAGAGTTTCCCGTCTGCT 328

Db 266 CTGAACAGCAGTCTCTCCACCCCTGGAGAACCTGATCTTAAATGAGTTTCTTATACGGCC 325
QY 301 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCACGAGCGCGTCTGCTCCAG 360
Db 326 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCACGAGCGCGTCTGCTCCAG 385
QY 361 CTGATTCAGGAACCGCTGCTGAGAGGATTTGATCAAGCGGGCTGATCTGATGGC 420
Db 386 CTGATTCAGGAACCGCTGCTGAGAGGATTTGATCAAGCGGGCTGATCTGATGGC 445
QY 421 ATCCCTGAGACCGCTGAGAGGCTTGAAGATTCAGACCTGGGATCACACCCAGACAC 480
Db 446 ATCCCTGAGACCGCTGAGAGGCTTGAAGATTCAGACCTGGGATCACACCCAGACAC 505
QY 481 GTCAATTTGCTGAGTGCTCCAGACACCGTCTGATCGAGAGAACTTGGGAGAGAAATC 540
Db 506 GTCAATTTGCTGAGTGCTCCAGACACCGTCTGATCGAGAGAACTTGGGAGAGAAATC 565
QY 541 GACCTCTCAAACTGGAGAGATTTATCAACACCTTTGACTGGCCACCCGATCTGAATC 600
Db 566 GACCTCTCAAACTGGAGAGATTTATCAACACCTTTGACTGGCCACCCGATCTGAATC 625
QY 601 CAGAACCGTCTCATGTCAGAGGACATCTCAGAGCTGGAGAGGCTCAGAACTGCTG 660
Db 626 CAGAACCGTCTCATGTCAGAGGACATCTCAGAGCTGGAGAGGCTCAGAACTGCTG 685
QY 661 GAGTATCATAGGAACATGTCAGAGGTCATTTCTCTTACCCCAAACTCTCAAGTCATC 720
Db 686 GAGTATCATAGGAACATGTCAGAGGTCATTTCTCTTACCCCAAACTCTCAAGTCATC 745
QY 721 AGTGTGACACGACATGTCAGAGTCTTCTTACAGAGGCTCTGACCTATGTCACCAAGCAAC 780
Db 746 AGTGTGACACGACATGTCAGAGTCTTCTTACAGAGGCTCTGACCTATGTCACCAAGCAAC 805
QY 781 CATCTGACTAATGCCCCGTTTACCCCGA--GGGTGCTGCTGCTGGGCTGCTGGGAGTGG 839
Db 806 CATCTGACTAATGCCCCGTTTACCCCGA--GGGTGCTGCTGCTGGGCTGCTGGGAGTGG 865
QY 840 GAAAGTCTGACAGCGCG--CGCTCTGCGCCAGAAATACA--GGTTGTCAATGTCTGCTGT 897
Db 866 GAAAGTCTGACAGCGCGCTCTCTGGGCAAGAAATACAGGGCTTGTCAATGTCTGCTGT 925
QY 898 GGGCAACTGCTGAAAG--AGGCTGTGCGCAGATAGGACACCGTTT--GGCGAGCTCATCCAG 954
Db 926 GGGGCACTGTGAAAGAAAGCTGTGGGCAATAGGACACCGTTTGGGGAGGTCATCCCG 985
QY 955 CCCTTT--CTTTGAAAGAGATGGCAGTTCTCTG--ACAGCTCTCATGAGTGC--TGAG 1010
Db 986 CCCTTTCTTTGTAAGGAAATGGGAGTTCTCTGACAGCTTCTCTGAGAGTGTCTTAC 1045
QY 1011 CCAGCGCTGAGACGAGGACTGATCCAGAAAGGCTGGTG 1053
Db 1046 CAAGCGCTTGGACACGAGCTGGCTCCCAAGGCTGGTG 1088

RESULT 4
CD515464

DEFINITION CD515464 886 bp mRNA linear EST 06-JUN-2003
AGENCY: 14364661 NIH MGC.181 Homo sapiens cDNA clone
IMAGE:30407307 5', mRNA sequence.

ACCESSION

CD515464

VERSION

CD515464.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 886)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Sequencing by: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM488 row: h column: 04
High quality sequence stop: 759.

FEATURES
source

1..886
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30407307"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH MGC 181"
/note="Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.9%; Score 805.6; DB 6; Length 886;
Best Local Similarity 98.8%; Pred. No. 6.3e-204;
Matches 824; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 1 ATGACGCCACTATCGCCCGCACCGTATCCCGCCGAGATGCCCGAGTACCGGAGGAG 60
Db 18 ATGACGCCACTATCGCCCGCACCGTATCCCGCCGAGATGCCCGAGTACCGGAGGAG 77
QY 61 AACCAATCTTCAGTTGATGAGAAATGTCGAGCAATCTCTGAGCAATCTGCGCCAGGAT 120
Db 78 AACCAATCTTCAGTTGATGAGAAATGTCGAGCAATCTCTGAGCAATCTGCGCCAGG 137
QY 121 GATCCATCCCTTCATGATCGAGCAATCTGATGAGCAATCTGATGAGCAATCTGCGCCAG 180
Db 138 GATCCATCCCTTCATGATCGAGCAATCTGATGAGCAATCTGATGAGCAATCTGCGCCAG 197
QY 181 GTAAATATAGGTCACCGCCCTCAGGGGAAACCAACATAGCAATGTGGCTCTGCAAAAT 240
Db 198 GTAAATATAGGTCACCGCCCTCAGGGGAAACCAACATAGCAATGTGGCTCTGCAAAAT 257
QY 241 CTGAACAGCAGTCTCTCTCACCCCTGGAGAACTGATCTTAAATGAGTTTCTTATACGGCC 300
Db 258 CTGAACAGCAGTCTCTCTCACCCCTGGAGAACTGATCTTAAATGAGTTTCTTATACGGCC 317
QY 301 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCACGAGCGCGCTGCTGTCAG 360
Db 318 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCACGAGCGCGCTGCTGTCAG 377
QY 361 CTGATTCAGAGACCGCTGGCTGAGAGAGATTTGATCAAGCGGGCTGAGATCTTGGATGGC 420
Db 378 CTGATTCAGAGACCGCTGGCTGAGAGAGATTTGATCAAGCGGGCTGAGATCTTGGATGGC 437
QY 421 ATCCCTGAGACCGCTGGCTGAGAGAGATTTGATCAAGCGGGCTGAGATCTTGGATGGC 480
Db 438 ATCCCTGAGACCGCTGGCTGAGAGAGATTTGATCAAGCGGGCTGAGATCTTGGATGGC 497
QY 481 GTCAATTTGCTGAGTGCTCCAGACACCGTCTCTGATCGAGAGAACTTGGGAGAGAAATC 540
Db 498 GTCAATTTGCTGAGTGCTCCAGACACCGTCTCTGATCGAGAGAACTTGGGAGAGAAATC 557
QY 541 GACCTCTCAAACTGGAGAGATTTATCAACACCTTTGACTGGCCACCCGATCTGAATC 600
Db 558 GACCTCTCAAACTGGAGAGATTTATCAACACCTTTGACTGGCCACCCGATCTGAATC 617

601 CAGAACCGTCTCATGTTGCGAGAGGACATCTCAGAGCTGAGACGGCTCAGAACTGCTG 660
618 CAGAACCGTCTCATGTTGCGAGAGGACATCTCAGAGCTGAGACGGCTCAGAACTGCTG 677
661 GAGTATCATAGGAACATCGTCAGGGTCATTCCTCTCTACCCCAAAATCTCAAAGTCATC 720
678 GAGTATCATAGGAACATCGTCAGGGTCATTCCTCTCTACCCCAAAATCTCAAAGTCATC 737
721 AGTCTGACGACCATGTTGGAGCTTTTACAGGCTGTGACCTGTGCTCGGGCCCTGCGG 833
738 AGTCTGACGACCATGTTGGAGCTTTTACAGGCTGTGACCTGTGCTCGGGCCCTGCGG 853
781 CATGCTACTAATGCCCCGTTTACCCCGAGGGGTGCTGCTCGGGCCCTGCGG 853
798 CATGCTACTAATGCCCCGTTTACCCCGAGGGGTGCTGCTCGGGCCCTGCGG 853

RESULT 5
BI19382 890 bp mRNA linear EST 04-OCT-2001
LOCUS 60303455F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:517575 5',
DEFINITION mRNA sequence.
ACCESSION BI19382
VERSION BI19382.1 GI:15930932
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 889.
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/clone="IMAGE:517575"
/lab_host="DH10B"
/clone_lib="NIH MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 54.4%; Score 783.2; DB 4; Length 890;
Best Local Similarity 98.0%; Pred. No. 6.2e-198;
Matches 825; Conservative 0; Mismatches 13; Indels 4; Gaps 3;
QY 1 ATGAGCCGCTATCGCCCGCAGCTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60
DB 53 ATGAGCCGCTATCGCCCGCAGCTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 112
QY 61 AACACATCTTCGAGTTGATGACAGAACATCTCGAGCAACTCTGTATCCACGACCGGAA 120

113 AACACATCTTCGAGTTGATGACAGAACATCTCGAGCAACTCTGTATCCACGACCGGAA 172
121 GATCCCATCCCTTTCATGATCCAGCACTTCATAGAGAACAAACATATGTGCCAGATT 180
173 GATCCCATCCCTTTCATGATCCAGCACTTCATAGAGAACAAACATATGTGCCAGGA-T 231
181 GTAATATTAAGTTCACCCGCTCAGGGAACAAACATATGTGGCTCTGCAACAT 240
232 GTAATATTAAGTTCACCCGCTCAGGGAACAAACATATGTGGCTCTGCAACAT 291
241 CTGAACACAGCTCTCTCACCCTCGAGAACCTGTATCTTAAATGAGTTTCTATACGGCC 300
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421 ATCCCTCGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTCTGGGGATCACACCCAGAC 480
472 ATCCCTCGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTCTGGGGATCACACCCAGAC 531
481 GTCAATTGCTGAGTGTCCAGACACGCTCTGATCCAGAGAACTTCGGGGAAGAGAATC 540
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541 GACCTTCAAACTGGAGAGATTTATCACACCACTTTGATCGCCACCCGAAATCTGAAATC 600
592 GACCTTCAAACTGGAGAGATTTATCACACCACTTTGATCGCCACCCGAAATCTGAAATC 651
601 CAGAACCGTCTCATGTTGCGAGAGGACATCTCAGAGCTGAGACGGCTCAGAACTGCTG 660
652 CAGAACCGTCTCATGTTGCGAGAGGACATCTCAGAGCTGAGACGGCTCAGAACTGCTG 711
661 GAGTATCATAGGAACATCTGAGGGTCATTCCTCTCTACCCCAAAATCTCAAAGTCATC 720
712 GAGTATCATAGGAACATCTGAGGGTCATTCCTCTCTACCCCAAAATCTCAAAGTCATC 771
721 AGTCTGACGACCATGTTGGAGCTTTCTACAGGCTCTGACCTATCTCAAAGCAAC 780
772 AGTCTGACGACCATGTTGGAGCTTTCTACAGGCTCTGACCTATGGTCAAAGC-AC 830
781 CATGCTACTAATGCCCCGTTTACCCCGAGGGGTGCTGCTCGGGCTCTGGGCGAGTGGG 840
831 CATGCTACTAATGCCCCGTTTACCCCGAGGGGTGCTGCTCGGGCTCTGGGCGAGTGGG 888
841 AA 842
889 AA 890

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DEFINITION AGENCOURT 6644707. NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5767090
5', mRNA sequence.
ACCESSION BM926674
VERSION BM926674.1 GI:19377053
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1130)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabps-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1824 row: m column: 11
 High quality sequence stop: 682.
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 /lab_host="DH10B"
 /clone_lib="NIH_MGC 122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 51.6%; Score 743.6; DB 5; Length 1130;
 Best Local Similarity 92.8%; Pred. No. 2.6e-187;
 Matches 862; Conservative 0; Mismatches 20; Indels 47; Gaps 6;

QY 1 ATGACGCCACTATCGCCGCGACCGTATCCCGCCGAGATGCCCGATCGGGGAGGAG 60
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 QY 61 AACCAATCTTCGAGTTGATG-----CAG 84
 DB 86 AACCAATCTTCGAGTTGATGACAGGATTAACCACTCGGGTGTCTGCGCTGCACCCACAG 145
 QY 85 AACATGCTGGAGCAATCTCTGATCCACAGCCGAGATCCCATCCCTTCATGATCCAG 144
 DB 146 AACATGCTGGAGCAATCTCTGATCCACAGCCGAGATCCCATCCCTTCATGATCCAG 205
 QY 145 CACTTGATAGACACACCAATGTCGCCAGGATTCATATATAGTCCACCGCCCTCA 204
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 QY 385 GAGGATTCATCAGCAGCGGCTGGATTCGATGGGATCCCTGAGCGCGTGCAGGCT 444
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 DB 566 ACSGTCTGATCAGAGAAACTTGGGGAAGAGATCGACCTCAAACTGGAGAGATTAT 625

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 QY 802 ACCCGCA---GGGTGCTGCTGCTCGGGCTGTGGG---CAGTGGGAAAAGTCTGCAGGCC 855
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 QY 856 --GCCCTCTCTGCGCCAGAAATACAGGCTT 882
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 LOCUS 603079308F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171185 5',
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 ACCESSION BI829572
 VERSION BI829572.1 GI:15941122
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>
 1 (bases 1 to 827)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabps-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 819.
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 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

FEATURES
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 1..827
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5171185"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC 119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match	50.2%;	Score 723.2;	DB 4;	Length 827;
Best Local Similarity	98.8%;	Pred. No. 6.7e-182;		
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QY	1	ATGGAGCGCACTATCGCCCC- GCACCGTATCCCGCGAGATGCCCGAGTACGGGGAGGA	59	
Db	18	ATGGAGCGCACTATCGCCCCGGACCGTATCCCGCGAGATGCCCGAGTACGGGGAGGA	77	
QY	60	GAACCACTCTTCGAGTTGATGCGAACAATGCTGGAGCAACTCTGTATCCACGAGCCGA	119	
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QY	120	AGATCCCATCCCTTCATGATCCAGCACTTCGATAGAGACAAAGACAAATGTGCCAGGAT	179	
Db	138	AGATCCCATCCCTTCATGATCCAGCACTTCGATAGAGACAAAGACAAATGTGCCAGGAT	197	
QY	180	TGTAATATTAGTCCACCCGCTCAGGGAACAAACATATAGCAATGTGGCTCTGCAACA	239	
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Db	737	CATCAGTGTGACACGCAATGTTGGAGCTTCTTACAGGGTCTGACCTATGTCCAAA	796	
QY	776	GCAACCATCGTACTAATGCCCGTTCACCCCG 807		
Db	797	GCAA- CATCGTACTAATGCCCGTTCACCCCG 827		
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DEFINITION				
603060841F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210003 5',				
mRNA sequence.				
BI767614				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Homo sapiens (human)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

1	(bases 1 to 710)			
NIH-MGC	http://mgc.nci.nih.gov/.			
National Institutes of Health,	Mammalian Gene Collection (MGC)			
Unpublished (1999)				
Contact:	Robert Strausberg, Ph.D.			
Email:	cgapbs-remail.nih.gov			
Tissue Procurement:	Life Technologies, Inc.			
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by:	Incyte Genomics, Inc.			
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
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High quality sequence stop:	710.			
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Query Match	48.8%;	Score 703;	DB 4;	Length 710;
Best Local Similarity	100.0%;	Pred. No. 1.6e-176;		
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QY	1	ATGGAGCGCACTATCGCCCCCGCACCGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG	60	
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QY	361	CTGATTTCAGGAAACCGCTGGCTGAAGAGGATTGTCATCAAGCAGGGCTGGATTCTGGATGGC	420	
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Db	428	ATCCCTGAGACCGGTGAGCAGGCTCTGTAGGATCCAGACCCCTGGGGATCACACCCAGACAC	487	
QY	481	GTCAATTGTCTGAGTGTCTCCAGACCGTCTCTGTATGTCGAGAGAAATCTGGGGAAGAGATC	540	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 710)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMLL at:
http://image.llnl.gov
Plate: LMLL1527 row: a column: 12
High quality sequence stop: 710.
Location/Qualifiers
1..710
/organism="Homo sapiens"
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/clone="IMAGE:5210003"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed, and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

FEATURES
Source

ORIGIN

Query Match		48.8%;	Score 703;	DB 4;	Length 710;
Best Local Similarity		100.0%;	Pred. No. 1.6e-176;		
Matches 703;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGAGCCCACTATCGCCCGGACCGTATCCCGCGAGATGCCCCAGTACGGGGAGGA	60		
Db	8	ATGGAGCCCACTATCGCCCGGACCGTATCCCGCGAGATGCCCCAGTACGGGGAGGA	67		
Qy	61	AACCACTATTCGAGTTGATGAGAACATGCTGGAGCAACTCTGATCCACGAGCCGAA	120		
Db	68	AACCACTATTCGAGTTGATGAGAACATGCTGGAGCAACTCTGATCCACGAGCCGAA	127		
Qy	121	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGACACACGACAAATGTGCCAGGAT	180		
Db	128	GATCCCATCCCTTTCATGATCCAGCACTTGCATAGACACACGACAAATGTGCCAGGAT	187		
Qy	181	GTAATATTAGTCCACCCGCTCAGGGAACAAACATAGCAATGTGGCTCTGCAAAACAT	240		
Db	188	GTAATATTAGTCCACCCGCTCAGGGAACAAACATAGCAATGTGGCTCTGCAAAACAT	247		
Qy	241	CTGAAACAGCAGTCTCTCTCACCCCTGGAGAACCTGATCTTAAATGAGTTTCTTATAGCGC	300		
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Qy	301	ACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCACGAGCGCTGCTCGTCCAG	360		
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Qy	361	CTGATTCAGGAAACCGCTGGCTGAAGAGGATTGATCAAGCAGGCGCTGGATTCTGGATGGC	420		
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Qy	421	ATCCCTGAGACGGCTGAGCAGGCTCTGAGGATCCAGACCTCGGGATCCACCCAGACAC	480		
Db	428	ATCCCTGAGACGGCTGAGCAGGCTCTGAGGATCCAGACCTCGGGATCCACCCAGACAC	487		
Qy	481	GTCAATTCGTGAGTGTCTCCAGACACGCTCTGATCCAGAGAACTTTGGGGAAGAGATC	540		

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QY 541 GACCTCAATCGGAGAGATTATCACACACCTTTGACTGGCCACCCGAAATCTGAATC 600
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Db 668 GAGTATCATAGGAACATCGTCAGGTCATTTCCCTCTACCCCA 710

RESULT 9

BI828586
LOCUS
DEFINITION 670 bp mRNA linear EST 04-OCT-2001
603078486F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170317 5',
mRNA sequence.
BI828586
VERSION
KEYWORDS
SOURCE EST. GI:15940136
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1423 row: k column: 22
High quality sequence stop: 670.

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Site 2: EcoRV (destroyed); RNA source normal medulla from
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cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-167; Length 670;
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 34 CCGAGATCCCCAGTACGGGAGAGAACACATTTGAGTTGATCGAGAACATCTG 93
Db 1 CCGAGATCCCCAGTACGGGAGAGAACACATTTGAGTTGATCGAGAACATCTG 60
QY 94 GAGCAATCTCTGATCCACAGCCGGAAGATCCCATCCCTTCATGATCCAGCACTTGCAT 153
Db 61 GAGCAATCTCTGATCCACAGCCGGAAGATCCCATCCCTTCATGATCCAGCACTTGCAT 120

QY 154 AGAGCAACGACAAATGTGGCCAGGATTTGTAATATTAGGTCCACCCGGCTCAGGGAAAAACA 213
Db 121 AGAGCAACGACAAATGTGGCCAGGATTTGTAATATTAGGTCCACCCGGCTCAGGGAAAAACA 180
QY 214 ACAATAGCAATGTGGCTCTCTGCAAAACATCTGAAACAGCAGTCTCCCTCACCCCTGGAGAACCTG 273
Db 181 ACAATAGCAATGTGGCTCTCTGCAAAACATCTGAAACAGCAGTCTCCCTCACCCCTGGAGAACCTG 240
QY 274 ATCTTAATAGTATTTTCTTATACGGCCACCGAGCCAGAGGCTTTATCTGCAAGGAAG 333
Db 241 ATCTTAATAGTATTTTCTTATACGGCCACCGAGCCAGAGGCTTTATCTGCAAGGAAG 300
QY 334 ACAGTTCCGACGGCTGCTGCTCAGCTGATTCAGGAACCGCTGGCTGAAGAGGATTGC 393
Db 301 ACAGTTCCGACGGCTGCTGCTCAGCTGATTCAGGAACCGCTGGCTGAAGAGGATTGC 360
QY 394 ATCAAGCAGGGCTGGATTCTGGATGGCATCCCTCAGACGGCTGAGCAGGCTCTGAGGATC 453
Db 361 ATCAAGCAGGGCTGGATTCTGGATGGCATCCCTCAGACGGCTGAGCAGGCTCTGAGGATC 420
QY 454 CAGACCTGGGGATCACACCAGACACCTGCTGATTCAGGAACCGCTGGCTGAAGAGGATTGC 513
Db 421 CAGACCTGGGGATCACACCAGACACCTGCTGATTCAGGAACCGCTGGCTGAAGAGGATTGC 480
QY 514 ATCCAGAGAACTTTGGGAGAGAGATCGACCTCAAACTGAGAGATTTATCACACACC 573
Db 481 ATCCAGAGAACTTTGGGAGAGAGATCGACCTCAAACTGAGAGATTTATCACACACC 540
QY 574 TTGACTGGCCACCCGAAATCTGAAATCCAGAACCGTCTCATGTGCGCAGAGCATCTCA 633
Db 541 TTGACTGGCCACCCGAAATCTGAAATCCAGAACCGTCTCATGTGCGCAGAGCATCTCA 600
QY 634 GAGCTGAGACGGCTCAGAAACTCTGGAGTATCATAGGAACATCTGAGGTCATTTCCC 693
Db 601 GAGCTGAGACGGCTCAGAAACTCTGGAGTATCATAGGAACATCTGAGGTCATTTCCC 660
QY 694 TCCTACCCCA 703
Db 661 TCCTACCCCA 670

RESULT 10

CV030269
LOCUS
DEFINITION 657 bp mRNA linear EST 20-AUG-2004
9331 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC034776, mRNA sequence.

CV030269
ACCESSION
VERSION
KEYWORDS
SOURCE EST. GI:51488510

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 657)

REFERENCE

1 (bases 1 to 657)
Rual J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,
Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,
Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,
Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,
Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M.
Human ORFome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press

TITLE

JOURNAL

COMMENT

Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidale@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers

Mon Mar 21 09:11:06 2005

FORWARD: ATGAGCCCACTATCGCC
BACKWARD: CAGGGGATTTCTTGGCAGG
Insert Length: 657 Std Error: 60.00
Plate: 11065 row: 11 column: E
Seq primer: ACTGGCGTGGTTTACACAGCTGCTGACTGGGAAC
High quality sequence start: 97
High quality sequence stop: 656
POLYA=No.

FEATURES
source
1. .657
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team. Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN
Query Match 45.6%; Score 656; DB 7; Length 657;
Best Local Similarity 99.8%; Pred. No. 5.8e-164;
Matches 656; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGCCCACTATCGCCCGCAGCGTATCCCCCGAGATGCCCGAGTACGGGAGGAG 60
DB 1 ATGAGCCCACTATCGCCCGCAGCGTATCCCCCGAGATGCCCGAGTACGGGAGGAG 60
QY 61 AACCATCTTCGAGTTCATGCAGAACATCTGTGAGCAACTCTGTATCCACCGCCGAA 120
DB 61 AACCATCTTCGAGTTCATGCAGAACATCTGTGAGCAACTCTGTATCCACCGCCGAA 120
QY 121 GATCCATCCCTTCATGATCAGACATCTGATAGAGCAACGACATGTGCCAGATT 180
DB 121 GATCCATCCCTTCATGATCAGACATCTGATAGAGCAACGACATGTGCCAGATT 180
QY 181 GTAATATTAGTTCACCGCCTCAGGAAACAAATAGCAATGTGCTCTGCAACAT 240
DB 181 GTAATATTAGTTCACCGCCTCAGGAAACAAATAGCAATGTGCTCTGCAACAT 240
QY 241 CTGAACAGAGCTCTCTCAACCTCGAGAACCTGATCTTAAATGATTTTCTATACGGCC 300
DB 241 CTGAACAGAGCTCTCTCAACCTCGAGAACCTGATCTTAAATGATTTTCTATACGGCC 300
QY 301 ACCGAAGCCAGAGGTTTATCTGAAAGGAGACAGTTCACGAGGCTGATGATGCGCAG 360
DB 301 ACCGAAGCCAGAGGTTTATCTGCAAGGAGACAGTTCACGAGGCTGATGATGCGCAG 360
QY 361 CTGATTCAGGACGCTGCTGAAGAGATTCATCAAGCAGGCTGATGATGCGATGCG 420
DB 361 CTGATTCAGGACGCTGCTGAAGAGATTCATCAAGCAGGCTGATGATGCGATGCG 420
QY 421 ATCCCTGAGACGGTGTGAGCAGGCTCTGAGATCCAGACCTGGGATCACCCAGACAC 480
DB 421 ATCCCTGAGACGGTGTGAGCAGGCTCTGAGATCCAGACCTGGGATCACCCAGACAC 480
QY 481 GTCAATGTGTGATGCTCCAGACAGTTCCTGATCGAGAGAACTTGGGGAAGAAATC 540
DB 481 GTCAATGTGTGATGCTCCAGACAGTTCCTGATCGAGAGAACTTGGGGAAGAAATC 540
QY 541 GACCTCAAACTGGAGAGATTATCACACCACTTTGACTGGCCACCCGAATCTGAATC 600
DB 541 GACCTCAAACTGGAGAGATTATCACACCACTTTGACTGGCCACCCGAATCTGAATC 600
QY 601 CAGAACCGTCTCATGTGCCAGAGACATCTCAGCTGGAGCGGCTCAGAACTG 657
DB 601 CAGAACCGTCTCATGTGCCAGAGACATCTCAGCTGGAGCGGCTCAGAACTG 657

RESULT 11
BU617945/c
LOCUS
DEFINITION
UI-H-DF0-beu-d-15-0-UI.s1 NCI CGAP.DF0 Homo sapiens cDNA clone
UI-H-DF0-beu-d-15-0-UI 3', mRNA sequence.
BU617945
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BU617945 721 bp mRNA linear EST 23-SEP-2002
UI-H-DF0-beu-d-15-0-UI.s1 NCI CGAP.DF0 Homo sapiens cDNA clone
UI-H-DF0-beu-d-15-0-UI 3', mRNA sequence.
BU617945
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .721
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-beu-d-15-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP.DF0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP.DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTACGCTC.
TAG TISSUE=Subchondral bone
TAG LIB=UI-H-DF0
TAG_SEQ=GTTAAGCGTC"

ORIGIN

Query Match 41.0%; Score 591; DB 5; Length 721;
Best Local Similarity 99.7%; Pred. No. 1.4e-146;
Matches 591; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 848 TGCAAGCCGCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTTCTGCTGTGGCAACTGC 907
DB 719 TGCAGGCGGCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTTCTGCTGTGGCAACTGC 650
QY 908 TGAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTCTTTGAA 967
DB 659 TGAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTCTTTGAA 600
QY 968 AGGAGATGGCAGTTCTTCAGACGCTCTCATGAGGTGCTGAGCCAGCGCTCGACAC 1027
DB 599 AGGAGATGGCAGTTCTTCAGACGCTCTCATGAGGTGCTGAGCCAGCGCTCGACAC 540
QY 1028 AGGACTCATCCAGAAAGGCTGGGTGTCTACCGCGCTCCCGGGGAGCTCGACCGAC 1087

Db 539 AGGACTGCATCCAGAAAGGCTGGGTGCTACACGGCTCCCGGGGACCTCCACAGGCAC 480
 QY 1088 ACCTGCTGAACCGCTGGGCTACAAATCCCAACAGGCTGTTTCTGTAATGTCATTG 1147
 Db 479 ACCTGCTGAACCGCTGGGCTACAAATCCCAACAGGCTGTTTCTGTAATGTCATTG 420
 QY 1148 ATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGCGGAAAGTACC 1207
 Db 419 ATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGCGGAAAGTACC 360
 QY 1208 ACCTCATGTAACGCCCTCCCAACAGGCTGAGATCCAGGCTCGCTCTGAGAAACCAA 1267
 Db 359 ACCTCATGTAACGCCCTCCCAACAGGCTGAGATCCAGGCTCGCTCTGAGAAACCAA 300
 QY 1268 AGGATGCTGAAGAGCAGGTCAAGCTGAAATGACCTGTTCTACAGGAATCCAGCTGACT 1327
 Db 299 AGGATGCTGAAGAGCAGGTCAAGCTGAAATGACCTGTTCTACAGGAATCCAGCTGACT 240
 QY 1328 TGGAGCAGTTGATGGGTGCGCCATCACCTCAATGGGACAGGACCCATACAGTCT 1387
 Db 239 TGGAGCAGTTGATGGGTGCGCCATCACCTCAATGGGACAGGACCCATACAGTCT 180
 QY 1388 TCGATATCATGAGAGTGGGATCAATTAATCCCTGCCCAAGAAATCCCTGA 1440
 Db 179 TCGAATATCATGAGAGTGGGATCAATTAATCCCTGCCCAAGAAATCCCTGA 127

RESULT 12 BQ016312/c

LOCUS
 DEFINITION UI-H-DT1-awb-f-10-0-UI.s1 NCI CGAP DT1 Homo sapiens cDNA clone IMAGE:5887113 3', mRNA sequence.

ACCESSION BQ016312
 VERSION EST.
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 685)

JOURNAL NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Cloning Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seg primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1..685
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5887113"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP DT1"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP DT1 is a normalized cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in Lennon. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated

to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTGG.

TAG TISSUE=lung metastatic chondrosarcoma
 TAG_LIB=UI-H-DT1
 TAG_SEQ=AACTGTTGG

ORIGIN

Query Match 38.0%; Score 547; DB 5; Length 685;
 Best Local Similarity 99.6%; Pred. No. 8.3e-135;
 Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 892 TGCTGTGGCAACTGCTGAAAGAGCTGTGGCAGATAGGACCACTGTTTGGCGAGCTCATC 951
 Db 675 TGCTGTGGCAACTGCTGAAAGAGCTGTGGCAGATAGGACCACTGTTTGGCGAGCTCATC 616
 QY 952 CAGCCCTTTCTTTGAAAAGAGATGCGAGTTCCTGACAGCTCTCTCATGAGTGTGAGC 1011
 Db 615 CAGCCCTTTCTTTGAAAAGAGATGCGAGTTCCTGACAGCTCTCTCATGAGTGTGAGC 556
 QY 1012 CAGCGCTTGACACGAGCAGCTGATCCAGAAAGGCTGGGTGTACACGGCTGCCGCG 1071
 Db 555 CAGCGCTTGACACGAGCAGCTGATCCAGAAAGGCTGGGTGTACACGGCTGCCGCG 496
 QY 1072 GACTCGACCAAGCTGCTGAAACCGCTGGGTCTAATCCCAACAGGCTGTTTTTC 1131
 Db 495 GACTCGACCAAGCTGCTGAAACCGCTGGGTCTAATCCCAACAGGCTGTTTTTC 436
 QY 1132 CTGAATGTGCAATTTGATTTCCATCATGAGCGCTGACTCTGAGAGAAATTCATCCAGT 1191
 Db 435 CTGAATGTGCAATTTGATTTCCATCATGAGCGCTGACTCTGAGAGAAATTCATCCAGT 376
 QY 1192 ACTGGGGAAGGTACCACCTCATGTACAGCCACCTCCACCATGGAGATCCAGCTCGC 1251
 Db 375 ACTGGGGAAGGTACCACCTCATGTACAGCCACCTCCACCATGGAGATCCAGCTCGC 316
 QY 1252 CTCTCGACCAAGCAAGTGTGAAAGAGAGGTCAGTCAAGTGAATGAGACTGTTCTAC 1311
 Db 315 CTCTCGACCAAGCAAGTGTGAAAGAGAGGTCAGTCAAGTGAATGAGACTGTTCTAC 256
 QY 1312 AGGAATCAGTGTGAGTGTGAGCAGTGTGTATGGTTCGGCCATCACCTCAATGGGAGCAG 1371
 Db 255 AGGAATCAGTGTGAGTGTGAGCAGTGTGTATGGTTCGGCCATCACCTCAATGGGAGCAG 196
 QY 1372 GACCCATACAGTCTTCGAATATCATCGAGTGGGATCATTAATCCCTGCCAGAA 1431
 Db 195 GACCCATACAGTCTTCGAATATCATCGAGTGGGATCATTAATCCCTGCCAGAA 136
 QY 1432 ATCCCTCTGA 1440
 Db 135 ATCCCTCTGA 127

RESULT 13

BY704667

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY704667 996 bp mRNA linear EST 16-DEC-2002
 musculus cDNA clone 1190002A17 5', mRNA sequence.

BY704667
 BY704667.1 GI:27115799

EST.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 996)

Oikarai, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nakaide, I., Osato, R., Saito, R., Suzuki, H., Yamana, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
Mizushima-Sugano.J., Nakai.K. and Sugano.S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..550
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/clone="TST00249"
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ORIGIN

Query Match 35.7%; Score 514.2; DB 5; Length 550;
Best Local Similarity 99.4%; Pred. No. 4.6e-126;
Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGAGCGCCACTATCGCCCGCCACCGGTATCCCCCGGAGATGCCCGAGTACGGGGAGGAG 60
DB 32 ATGGAGCGCCACTATCGCCCGCCACCGGTATCCCCCGGAGATGCCCGAGTACGGGGAGGAG 91
QY 61 AACCAATCTTCGAGTTGATGCAGACATGCTGGAGCAATCTGATCCAGCCAGCCGAA 120
DB 92 AACCAATCTTCGAGTTGATGCAGACATGCTGGAGCAATCTGATCCAGCCAGCCGAA 151
QY 121 GATCCATCCCTTCATGATCGAGCATCTGCAATAGAGCAACAGCAATGTGCCAGGATT 180
DB 152 GATCCATCCCTTCATGATCGAGCATCTGCAATAGAGCAACAGCAATGTGCCAGGATT 211
QY 181 GTAATATTAGTTCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAAT 240
DB 212 GTAATATTAGTTCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAAT 271
QY 241 CTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATAGATTTCCTATAGGCC 300
DB 272 CTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATAGATTTCCTATAGGCC 331
QY 301 ACCGAGCGCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGGCTGCTCTCCAG 360
DB 332 ACCGAGCGCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGGCTGCTCTCCAG 391
QY 361 CTGATTGAGAAACGCTGCTGAGAGGATTGCATCAAGCAGGCTGGATTCTGGATGCC 420
DB 392 CTGATTGAGAAACGCTGCTGAGAGGATTGCATCAAGCAGGCTGGATTCTGGATGCC 451
QY 421 ATCCCTGAGACGCGTGCAGAGGCTCTGAGGATCAGACCTGGGGATCACCCAGACAC 480
DB 452 ATCCCTGAGACGCGTGCAGAGGCTCTGAGGATCAGACCTGGGGATCACACTCAGAC 511
QY 481 GTCAATTGTGCTGAGTCTCCACACGCTCTGATCGAG 519
DB 512 GTCAATTGTGCTGAGTCTCCACACGCTCTGATCGAG 550

RESULT 15

BP347783
LOCUS BP347783 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION 583 bp mRNA linear EST 17-SEP-2004
S2B06383, mRNA sequence.
ACCESSION BP347783
VERSION BP347783.1
KEYWORDS BP347783.1 GI:52277768
EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
Mizushima-Sugano.J., Nakai.K. and Sugano.S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZB06383"
/tissue_type="brain"
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ORIGIN

Query Match 35.7%; Score 513.8; DB 5; Length 583;
Best Local Similarity 98.9%; Pred. No. 8e-126;
Matches 548; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
QY 1 ATGGAACCCACTAT-CCGCCCGCACCGTATCCCCCGGAGATGCCCGAGTACGGGGAGGA 59
DB 30 ATGGAACCCACTATAGCCCGCCGACCGTATCCCCCGGAGATGCCCGAGTACGGGGAGGA 89
QY 60 GAACCAATCTTCGAGTTGATGCAGAAATCTCTGGAGCAATCTCTGATCCACAGCCGGA 119
DB 90 GAACCAATCTTCGAGTTGATGCAGAAATCTCTGGAGCAATCTCTGATCCACAGCCGGA 149
QY 120 AGATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAACAGCAATGTGCCAGGAT 179
DB 150 AGATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAACAGCAATGTGCCAGGAT 209
QY 180 TGTAAATTAGTTCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAACA 239
DB 210 TGTAAATTAGTTCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAACA 269
QY 240 TCTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAAATGAGTTTCTTATACGCC 299
DB 270 TCTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAAATGAGTTTCTTATACGCC 329
QY 300 CACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGATTCCCGAGCGGCTGCTCGTCCA 359
DB 330 CACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGATTCCCGAGCGGCTGCTCGTCCA 389
QY 360 GCTGATTTCAGGAACCGCTGGCTGAAGAGGATTCG-ATCAAGCAGGG-CTGGATTCTGGAT 417
DB 390 GCTGATTTCAGGAACCGCTGGCTGAAGAGGATTCGATCAAGCAGGAGCTGGATTCTGGAT 449
QY 418 GGCATCTCTGAGACCGCTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGA 477
DB 450 GGCATCTCTGAGACCGCTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGA 509
QY 478 CACGTCAATTGTCTGAGTCTCCAGACACCGTCTCTGATCGAGAGAACTTGGGGAAGAGA 537
DB 510 CACGTCAATTGTCTGAGTCTCCAGACACCGTCTCTGATCGAGAGAACTTGGGGAAGAGA 569
QY 538 ATCGACCTCTCAAC 551
DB 570 ATCGACCTCTCANAC 583

Search completed: March 19, 2005, 23:48:58
Job time : 4394 sec

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Mon Mar 21 09:11:05 2005

CC activity and polynucleotides encoding them. The polynucleotides, proteins, antibodies, agonists and antagonists of the proteins are useful for drug screening, clinical trial monitoring, and diagnosis or treating diseases or disorders associated with biological disorders or imbalances. The proteins and polynucleotides are useful in cosmetic and nutraceutical applications, for identifying protein coding sequences and mapping a unique gene to a particular chromosome. The sequence of the polynucleotides and proteins can also be used as additional DNA markers for restriction fragment length polymorphism analysis, or in forensic biology. The present sequence represents a NHP kinase encoding DNA

XX
SQ Sequence 1440 BP; 368 A; 419 C; 367 G; 286 T; 0 U; 0 Other;

Query Match 100.0%; Score 1440; DB 10; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGCCACTATCGCCCGCCGACCGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60
Db 1 ATGAGCGCCACTATCGCCCGCCGACCGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60
QY 61 AACACATCTTCGAGTTGATGACAGACATGCTGGAGCACTCTCTGATCCACACCGCCGAA 120
Db 61 AACACATCTTCGAGTTGATGACAGACATGCTGGAGCACTCTCTGATCCACACCGCCGAA 120
QY 121 GATCCCATCCCTTCATGATCCAGCACTTGATAGAGACACAGCAATGTGCCAGGATT 180
Db 121 GATCCCATCCCTTCATGATCCAGCACTTGATAGAGACACAGCAATGTGCCAGGATT 180
QY 181 GTAATATTAGTTCACCGCCCTCAGGGAAACAAACAATAGCAATGTGGCTCTGCAACAT 240
Db 181 GTAATATTAGTTCACCGCCCTCAGGGAAACAAACAATAGCAATGTGGCTCTGCAACAT 240
QY 241 CTGAACAGAGTCTCTCACCCTGGAGAACCTGATCTTAATAGATTTTCTATACGGCC 300
Db 241 CTGAACAGAGTCTCTCACCCTGGAGAACCTGATCTTAATAGATTTTCTATACGGCC 300
QY 301 ACCGAAGCCAGAGGCTTTATCTGCAAGAGAGACAGTTCACGCGGCTCTCGTCCAG 360
Db 301 ACCGAAGCCAGAGGCTTTATCTGCAAGAGAGACAGTTCACGCGGCTCTCGTCCAG 360
QY 361 CTGATTCAGGAACGGCTGGCTGAAGAGATTCATCAGCAGGGCTGGATTCTCGATGGC 420
Db 361 CTGATTCAGGAACGGCTGGCTGAAGAGATTCATCAGCAGGGCTGGATTCTCGATGGC 420
QY 421 ATCCCTTGACACGCTGAGCAGGCTCTGAGGATCCAGACCCCTGGGATCACACCCAGAC 480
Db 421 ATCCCTTGACACGCTGAGCAGGCTCTGAGGATCCAGACCCCTGGGATCACACCCAGAC 480
QY 481 GTCAATGTCTGAGTCTCCAGACACGGTCTGTATCGAGAACTTGGGAGAGATC 540
Db 481 GTCAATGTCTGAGTCTCCAGACACGGTCTGTATCGAGAACTTGGGAGAGATC 540
QY 541 GACCCCTCAAACTGGAGAGTTTATCACACACCTTTGACTGCCACCCGATCTGAATC 600
Db 541 GACCCCTCAAACTGGAGAGTTTATCACACACCTTTGACTGCCACCCGATCTGAATC 600
QY 601 CAGAACCGTCTCATGCTGCGCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGTG 660
Db 601 CAGAACCGTCTCATGCTGCGCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGTG 660
QY 661 GAGTATCATAGGAACATCGTCAGGGTCATTCCTACCCCAAAATCTCAAGTCATC 720
Db 661 GAGTATCATAGGAACATCGTCAGGGTCATTCCTACCCCAAAATCTCAAGTCATC 720
QY 721 AGTGTCTGACAGCAGTGTGGAGCTCTTCTACAGGCTCTGACCTATGTCCTCAAGCAAC 780
Db 721 AGTGTCTGACAGCAGTGTGGAGCTCTTCTACAGGCTCTGACCTATGTCCTCAAGCAAC 780
QY 781 CATCGTACTAATGCCCGGTTTACCCCGAGGGTCTGCTGGGGCTGTGGGAGTGGG 840
Db 781 CATCGTACTAATGCCCGGTTTACCCCGAGGGTCTGCTGGGGCTGTGGGAGTGGG 840

QY 841 AAAAGTCTGAGCGCGCCCTCTCTGGCCCAAGATACAGGCTTCAATGCTCTCTGTGGG 900
Db 841 AAAAGTCTGAGCGCGCCCTCTCTGGCCCAAGATACAGGCTTCAATGCTCTCTGTGGG 900
QY 901 CAATCTGCTGAAAGAGGCTGTGGCAGATAGGACACACGTTTGGCGAGCTCATCCAGCCCTTC 960
Db 901 CAATCTGCTGAAAGAGGCTGTGGCAGATAGGACACACGTTTGGCGAGCTCATCCAGCCCTTC 960
QY 961 TTTGAAAGAGGATGGGAGTTCCTGACAGCTCTCTATGAAGTGTGAGCCAGCGCTG 1020
Db 961 TTTGAAAGAGGATGGGAGTTCCTGACAGCTCTCTATGAAGTGTGAGCCAGCGCTG 1020
QY 1021 GACCAGCAGGACTGCATCCAGAAAGGCTGGTGTGTACACGCGCTCCCGCGGACCTCGAC 1080
Db 1021 GACCAGCAGGACTGCATCCAGAAAGGCTGGTGTGTACACGCGCTCCCGCGGACCTCGAC 1080
QY 1081 CAGGCACACCTGCTGAACCGCTGGGCTTACAATCCCAACAGGGTGTCTTCTGAATGTG 1140
Db 1081 CAGGCACACCTGCTGAACCGCTGGGCTTACAATCCCAACAGGGTGTCTTCTGAATGTG 1140
QY 1141 CCATTTGATTCATCATGAGGAGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
Db 1141 CCATTTGATTCATCATGAGGAGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
QY 1201 AGGTACCACTCATGTACAGCCACTCCACCATGGAGATCCAGGCTCGCTCTCGAG 1260
Db 1201 AGGTACCACTCATGTACAGCCACTCCACCATGGAGATCCAGGCTCGCTCTCGAG 1260
QY 1261 AACCCAAAGGATGCTGAAGAGCAGGTCAAGCTGAAATGAGACCTGTTCTACAGNACTCA 1320
Db 1261 AACCCAAAGGATGCTGAAGAGCAGGTCAAGCTGAAATGAGACCTGTTCTACAGNACTCA 1320
QY 1321 GCTGACTTGGAGCAGTGTGATGGTGGCCATCACCTCAATGGGACACAGACCCATAC 1380
Db 1321 GCTGACTTGGAGCAGTGTGATGGTGGCCATCACCTCAATGGGACACAGACCCATAC 1380
QY 1381 ACAGTCTTCCAAATACATCGAGAGTGGGATCATTAATCCCTGCCCAAGAAATCCCTTGA 1440
Db 1381 ACAGTCTTCCAAATACATCGAGAGTGGGATCATTAATCCCTGCCCAAGAAATCCCTTGA 1440

RESULT 2

ADAS3813
ID ADAS3813 standard; cDNA; 1579 BP.
XX ADAS3813;
AC ADAS3813;
XX
DT 20-NOV-2003 (first entry)
XX
XX Human coding sequence, SEQ ID 1381.

Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
Gene Therapy; human; secretory protein; membrane proteins; cancer;
inflammatory disease; osteoporosis; neurological disease; gene; ss.

Homo sapiens.

EP1293569-A2.

19-MAR-2003.

21-MAR-2002; 2002EP-00006586.

14-SEP-2001; 2001JP-00328381.

24-JAN-2002; 2002US-0350435P.

(HELI-) HELIX RES INST.

(REAS-) RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

DR WPI, 2003-395539/38.
XX P-PSDB; ADA5452.
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
XX which the gene is involved, or as target molecules for gene therapy.
XX Claim 1; SEQ ID NO 1381; 205bp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 1579 BP; 403 A; 467 C; 406 G; 303 T; 0 U; 0 Other;
Query Match 100.0%; Score 1440; DB 10; Length 1579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACGCCACTATCGCCCGCCACCGTATCCCGCCCGAGATGCCCGAGTACGGGAGGAG 60
DB 30 ATGGACGCCACTATCGCCCGCCACCGTATCCCGCCCGAGATGCCCGAGTACGGGAGGAG 89
QY 61 AACCAATCTTCGAGTTGATGACAGAACATGCTGGAGCACTCTGATCCACCGCCGAA 120
DB 90 AACCAATCTTCGAGTTGATGACAGAACATGCTGGAGCACTCTGATCCACCGCCGAA 149
QY 121 GATCCCATCCCTTCATGATCAGCACTTGATGATGAGCAACATGTCGCCAGGATT 180
DB 150 GATCCCATCCCTTCATGATCAGCACTTGATGATGAGCAACATGTCGCCAGGATT 209
QY 181 GTAATATTAGTTCACCCGCTCAGGGAACCAATAGCAATGTCGCAACAT 240
DB 210 GTAATATTAGTTCACCCGCTCAGGGAACCAATAGCAATGTCGCAACAT 269
QY 241 CTGAACAGCAGTCTCTCCCTCAGGAGACCTGATCTTAATGAGTTTCTTATAGGCC 300
DB 270 CTGAACAGCAGTCTCTCCCTCAGGAGACCTGATCTTAATGAGTTTCTTATAGGCC 329
QY 301 ACCGAGCCAGAGGCTTTATCTGCAAGGAGACAGTCTCCAGCGGCTGCTGTCAG 360
DB 330 ACCGAGCCAGAGGCTTTATCTGCAAGGAGACAGTCTCCAGCGGCTGCTGTCAG 389
QY 361 CTGATTGAGAACGCTTGGTGAAGGATTCATCAAGCAGGCTGGATTCTGATGGC 420
DB 390 CTGATTGAGAACGCTTGGTGAAGGATTCATCAAGCAGGCTGGATTCTGATGGC 449
QY 421 ATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCAGACCTCGGGATCACCCAGAC 480
DB 450 ATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCAGACCTCGGGATCACCCAGAC 509
QY 481 GTCAATGCTGAGTCTCCACACAGGCTCTGATCGAGAGAACTTGGGAGAGAAATC 540
DB 510 GTCAATGCTGAGTCTCCACACAGGCTCTGATCGAGAGAACTTGGGAGAGAAATC 569
QY 541 GACCTCAAACTGGAGAGATTATCAACACCTTTGACTGGCCACCGGAATCTGAAATC 600
DB 570 GACCTCAAACTGGAGAGATTATCAACACCTTTGACTGGCCACCGGAATCTGAAATC 629
QY 601 CAGAACCGTCTCATGGTGCAGAGACATCTCGAGAGCTGGAGACGGCTCAGAAATCTG 660
DB 630 CAGAACCGTCTCATGGTGCAGAGACATCTCGAGAGCTGGAGACGGCTCAGAAATCTG 689
QY 661 GAGTATCATAGGAACATCGTCAAGGTCATTCTCTACCCCAAAATCTCAAGTCAATC 720
DB 690 GAGTATCATAGGAACATCGTCAAGGTCATTCTCTACCCCAAAATCTCAAGTCAATC 749
QY 721 AGTGCTGACCGCATGTTGGAGCTTCTTACAGGCTCTGACCTATGTCAAAGCAAC 780
DB 750 AGTGCTGACCGCATGTTGGAGCTTCTTACAGGCTCTGACCTATGTCAAAGCAAC 809

QY 781 CATCTACTAATGCCCCGTTTACCCGAGGGTGTCTGCTCGGGCCCTGTGGGCACTGCG 840
DB 810 CATCTACTAATGCCCCGTTTACCCGAGGGTGTCTGCTCGGGCCCTGTGGGCACTGCG 869
QY 841 AAAAGTCTGAGGCGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGGG 900
DB 870 AAAAGTCTGAGGCGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGGG 929
QY 901 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCACTTTGGCAGGCTCATCCAGCCCTTC 960
DB 930 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCACTTTGGCAGGCTCATCCAGCCCTTC 989
QY 961 TTTGAAAAGAGGATGGCAGTTCCTGACAGCCCTCTCATGAGGTGTGGAGCGAGCCCTG 1020
DB 990 TTTGAAAAGAGGATGGCAGTTCCTGACAGCCCTCTCATGAGGTGTGGAGCGAGCCCTG 1049
QY 1021 GACCAGCAGGACTGCATCCAGAAAGCTGGGTGTCTACAGGCGTCCCGGGGACCTCGAC 1080
DB 1050 GACCAGCAGGACTGCATCCAGAAAGCTGGGTGTCTACAGGCGTCCCGGGGACCTCGAC 1109
QY 1081 CAGGACACCTGCTGAAACCGCCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGTG 1140
DB 1110 CAGGACACCTGCTGAAACCGCCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGTG 1169
QY 1141 CCATTGATTTCCATCATGAGGCGGCTGACTCTGAGAAAGAAATTCATCCAGTCACTGGGAA 1200
DB 1170 CCATTGATTTCCATCATGAGGCGGCTGACTCTGAGAAAGAAATTCATCCAGTCACTGGGAA 1229
QY 1201 AGGTACCACCTCATGTACAGCCACCTCCACCATGGAGATCCAGGCTCGCTCTGCGAG 1260
DB 1230 AGGTACCACCTCATGTACAGCCACCTCCACCATGGAGATCCAGGCTCGCTCTGCGAG 1289
QY 1261 AACCCAAAGATGCTGAGAGCAGGCTCAAGCTGAAATGGAATCTTCTACAGGAATCTCA 1320
DB 1290 AACCCAAAGATGCTGAGAGCAGGCTCAAGCTGAAATGGAATCTTCTACAGGAATCTCA 1349
QY 1321 GCTGACTTGGAGCAGTGTGTATGGGTTCGGCCATCACTCAATGGGAGCCAGGACCCATAC 1380
DB 1350 GCTGACTTGGAGCAGTGTGTATGGGTTCGGCCATCACTCAATGGGAGCCAGGACCCATAC 1409
QY 1381 ACAGTCTTCGAATACATCGAGAGTGGGATCATTAATCCCTGCCCAAGAAATCCCTGA 1440
DB 1410 ACAGTCTTCGAATACATCGAGAGTGGGATCATTAATCCCTGCCCAAGAAATCCCTGA 1469
RESULT 3
AAD53173
ID AAD53173 standard; cDNA; 1581 BP.
XX
AC AAD53173;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human kinases and phosphatases (KPP)-3 cDNA.
XX
KW Human; kinase and phosphatase; KPP; enzyme; cardiovascular disorder;
XX neurological disorder; cancer; gene therapy; gene; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 15..1454
FT /*tag= a
FT /product= "KPP protein"
XX
XX MO200294780-A2.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2002; 2002WO-US016634.
XX
XX 24-MAY-2001; 2001US-0293665P.
XX
XX 15-JUN-2001; 2001US-0298712P.

PR 06-JUL-2001; 2001US-0303418P.
PR 19-JUL-2001; 2001US-0306967P.
PR 27-JUL-2001; 2001US-0308183P.
PR 15-DEC-2001; 2001US-0343007P.
PR 15-FEB-2002; 2002US-0357675P.
PR 30-APR-2002; 2002US-0376988P.
XX (INCY-) INCVTE GENOMICS INC.
XX Yue H, Lu DAM, Azimzai Y, Ding L, Lee EA, Hafalia AJA, Becha SD;
XX Tang YT, Lal PG, Griffin JA, Gururajan R, Ramkumar J, Elliott VS;
XX Arvizu CS, Luo W, Swarnakar A, Duggan BM, Tran UK, Walia NK;
XX Gandhi AR, Yao MG, Khan FA, Raughn WR, Borowsky ML, Zebarjadian Y;
XX Richardson TW, Marquis JP, Chien D, Jin P;
XX WPI; 2003-120774/11.
XX P-PSDB; AAE34860.
XX New human kinases and phosphatases (KPP), useful for preparing a
XX composition for diagnosing or treating a disease or condition associated
XX with decreased expression or overexpression of functional KPP e.g.,
XX cancer.
XX Claim 5; Col 154; 82pp; English.
XX The invention relates to novel human kinases and phosphatases (KPP)
XX polypeptides and polynucleotides. Polypeptides of the invention are used
XX for screening agonists and antagonists. They are used to make monoclonal
XX or polyclonal or antibodies, which are used in diagnostic tests for
XX conditions or diseases associated with expression of the polypeptide.
XX They are also useful for diagnosing or treating diseases or conditions
XX associated with decreased expression or overexpression of functional KPP
XX e.g. cardiovascular or neurological disorders or cancer. The invention is
XX useful in gene therapy. The present sequence is human KPP cDNA
XX
SQ Sequence 1581 BP; 413 A; 464 C; 402 G; 302 T; 0 U; 0 Other;
Query Match 100.0%; Score 1440; DB 8; Length 1581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGCGCATTATGCGCCGCGCAGCTATCCCGCGAGATGCCAGTACGGGGAGG 60
DB 15 ATGGAGCGCATTATGCGCCGCGCAGCTATCCCGCGAGATGCCAGTACGGGGAGG 74
QY 61 AACCATCTCTCGAGTTGATGAGAACATCTGCGAGCACTCTGATCCACCGCCGAA 120
DB 75 AACCATCTCTCGAGTTGATGAGAACATCTGCGAGCACTCTGATCCACCGCCGAA 134
QY 121 GATCCCATCCCTTCATGATCCAGCATCTGCGATGAGAACAGCAATGTGCCAGGATT 180
DB 135 GATCCCATCCCTTCATGATCCAGCATCTGCGATGAGAACAGCAATGTGCCAGGATT 194
QY 181 GTAAATATTAGTCCACCGCCCTCAGGAAACAAATAGCAATGTGGCTCTGCAAAAT 240
DB 195 GTAAATATTAGTCCACCGCCCTCAGGAAACAAATAGCAATGTGGCTCTGCAAAAT 254
QY 241 CTGAACAGCAGTCTCTCCCTCCCTGGAGAACCTGATCTTAAATGAGTTTCTATACGCC 300
DB 255 CTGAACAGCAGTCTCTCCCTCCCTGGAGAACCTGATCTTAAATGAGTTTCTATACGCC 314
QY 301 ACCGAGCCGAGAGGCTTTATCTGCAAGAGAGAGTTCACGCGCGCTGCTGCTCCAG 360
DB 315 ACCGAGCCGAGAGGCTTTATCTGCAAGAGAGAGTTCACGCGCGCTGCTGCTCCAG 374
QY 361 CTGATTCAGGAACGCTTGCTGAGAGGATTGATCAAGCAGCGCTGGATTCTGATGCG 420
DB 375 CTGATTCAGGAACGCTTGCTGAGAGGATTGATCAAGCAGCGCTGGATTCTGATGCG 434
QY 421 ATCCCTCAGACGGCTGAGAGGCTCTGAGGATCCAGACCTGGGGATCACCCAGACAC 480
DB 435 ATCCCTCAGACGGCTGAGAGGCTCTGAGGATCCAGACCTGGGGATCACCCAGACAC 494

QY 481 GTCAATTGCTGAGTGTCTCAGACACGGTCTCTGATCGAGAGAACTTGGGAGAGAAATC 540
DB 495 GTCAATTGCTGAGTGTCTCAGACACGGTCTCTGATCGAGAGAACTTGGGAGAGAAATC 554
QY 541 GACCTCAAACTGGAGAGATTATACACCACTTTGACTGGCCACCCGAATCTGAAATC 600
DB 555 GACCTCAAACTGGAGAGATTATACACCACTTTGACTGGCCACCCGAATCTGAAATC 614
QY 601 CAGAACCGTCTCATGGTCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 660
DB 615 CAGAACCGTCTCATGGTCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 674
QY 661 GAGTATCATAGGACATCTGCTGAGGCTCATCTCCCTCTACCCCAAAATCTCAAAGTCA 720
DB 675 GAGTATCATAGGACATCTGCTGAGGCTCATCTCCCTCTACCCCAAAATCTCAAAGTCA 734
QY 721 AGTCTGTACACCGCATGTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCA 780
DB 735 AGTCTGTACACCGCATGTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCA 794
QY 781 CATCTACTAATGCCCCCTTCAACCCGAGGCTGCTGCTCCGGCGCTGTGGCGAGTGGG 840
DB 795 CATCTACTAATGCCCCCTTCAACCCGAGGCTGCTGCTCCGGCGCTGTGGCGAGTGGG 854
QY 841 AAAAGTCTGACGGCGCGCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGTTGG 900
DB 855 AAAAGTCTGACGGCGCGCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGTTGG 914
QY 901 CAACTGCTGAAAGAGGCTGTGCGAGATAGGACCGAGTTTGGCGAGCTCATCCAGCCCTTC 960
DB 915 CAACTGCTGAAAGAGGCTGTGCGAGATAGGACCGAGTTTGGCGAGCTCATCCAGCCCTTC 974
QY 961 TTTGAAAGAGGAGATGGCGAGTCTCTGACAGCTCTCTCATGAAGTGTCTGAGCAGCGCTG 1020
DB 975 TTTGAAAGAGGAGATGGCGAGTCTCTGACAGCTCTCTCATGAAGTGTCTGAGCAGCGCTG 1034
QY 1021 GACACGAGGACTGCATCCAGAAAGGCTGGGTGTCTACACGGCTCTCCGGGAGACTCGAC 1080
DB 1035 GACACGAGGACTGCATCCAGAAAGGCTGGGTGTCTACACGGCTCTCCGGGAGACTCGAC 1094
QY 1081 CAGGCAACCTGCTGAAACCGCTGGGTACATCCCAAGAGGCTGTTTCTGTAATGTG 1140
DB 1095 CAGGCAACCTGCTGAAACCGCTGGGTACATCCCAAGAGGCTGTTTCTGTAATGTG 1154
QY 1141 CCATTTGATTCCATCATGAGGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
DB 1155 CCATTTGATTCCATCATGAGGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1214
QY 1201 AGGTACCACTCATGTAAGCACTCTCCCACTGGAGATCCAGGCTCGCTCTGTCAG 1260
DB 1215 AGGTACCACTCATGTAAGCACTCTCCCACTGGAGATCCAGGCTCGCTCTGTCAG 1274
QY 1261 AACCCAAAGGATCTCAAGAGCAGGCTCAAGCTGAAATGGAGCTGTTCTACAGGAATCA 1320
DB 1275 AACCCAAAGGATCTCAAGAGCAGGCTCAAGCTGAAATGGAGCTGTTCTACAGGAATCA 1334
QY 1321 GCTGACTTTGAGCAGTGTGATGGGTGGGCAATCCCTCAATGGGACACGAGCCCATAC 1380
DB 1335 GCTGACTTTGAGCAGTGTGATGGGTGGGCAATCCCTCAATGGGACACGAGCCCATAC 1394
QY 1381 ACAGTCTTCAATACATCGAGAGTGGGATCATTAATCCCTGCGCCCAAGAAATCCCTCTGA 1440
DB 1395 ACAGTCTTCAATACATCGAGAGTGGGATCATTAATCCCTGCGCCCAAGAAATCCCTCTGA 1454

RESULT 4
ADC10109 standard; DNA; 1623 BP.
XX
XX ADC10109;
XX
XX 18-DEC-2003 (first entry)
XX

DE Human NOVX polypeptide coding sequence SEQ ID NO: 129.

XX ds; gene; cytostatic; antidiabetic; anorectic; cerebroprotective;
KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;
KW thymimetic; NOVX; pathology; cancer; diabetes; obesity;
KW endocrine disorder; CNS disorder; inflammatory disorder;
KW chromosome mapping; tissue typing; predictive medicine.
XX Homo sapiens.
XX MO2003000842-A2.
XX 03-JAN-2003.
XX 04-JUN-2002; 2002WO-US017443.
XX 04-JUN-2001; 2001US-0295607P.
XX 06-JUN-2001; 2001US-0295661P.
XX 06-JUN-2001; 2001US-0296404P.
XX 07-JUN-2001; 2001US-0296418P.
XX 11-JUN-2001; 2001US-0296575P.
XX 12-JUN-2001; 2001US-0297414P.
XX 12-JUN-2001; 2001US-0295573P.
XX 14-JUN-2001; 2001US-0297567P.
XX 15-JUN-2001; 2001US-0298285P.
XX 18-JUN-2001; 2001US-0298528P.
XX 19-JUN-2001; 2001US-0299133P.
XX 21-JUN-2001; 2001US-0299230P.
XX 22-JUN-2001; 2001US-029949P.
XX 22-JUN-2001; 2001US-0300177P.
XX 26-JUN-2001; 2001US-0300883P.
XX 28-JUN-2001; 2001US-0301530P.
XX 28-JUN-2001; 2001US-0301550P.
XX 03-JUL-2001; 2001US-0302951P.
XX 31-JUL-2001; 2001US-0308890P.
XX 14-SEP-2001; 2001US-0322297P.
XX 25-SEP-2001; 2001US-0324669P.
XX 03-DEC-2001; 2001US-0337477P.
XX 14-DEC-2001; 2001US-0341562P.
XX 21-FEB-2002; 2002US-0358656P.
XX 21-FEB-2002; 2002US-0359122P.
XX 22-FEB-2002; 2002US-0358978P.
XX 22-FEB-2002; 2002US-0359034P.
XX 22-FEB-2002; 2002US-0359121P.
XX 27-FEB-2002; 2002US-0359353P.
XX 01-MAR-2002; 2002US-0359964P.
XX 12-MAR-2002; 2002US-0360858P.
XX 12-MAR-2002; 2002US-0363430P.
XX 10-APR-2002; 2002US-0363676P.
XX 10-MAY-2002; 2002US-0371346P.
XX 04-JUN-2002; 2002US-0379444P.
XX (CURA-) CURAGEN CORP.
XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton B;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VA, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigar M, Patturajan M, Pena CE, Rastelli L, Rieser DK;
PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DW;
XX WPI; 2003-210149/20.
XX P-PSDB; ADC10110.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Claim 20; SEQ ID NO 129; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to the coding sequence
CC for one of the polypeptides of the invention.
XX
SQ Sequence 1623 BP; 409 A; 482 C; 419 G; 313 T; 0 U; 0 Other;
Query Match 96.8%; Score 1394; DB 10; Length 1623;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 1 ATGGAGCCCACTATCGCCCGCAGCCGATATCCCGCCGAGATGCCCGAGTACGGGGAGGAG 60
Db 38 ATGGAGCCCACTATCGCCCGCAGCCGATATCCCGCCGAGTACGGGGAGGAG 97
QY 61 AACCAACATCTTCGAGTTGATG-----CAG 84
Db 98 AACCAACATCTTCGAGTTGATGAGGATTAACCACTGGGTGTCTGCCCTGCCACCCAG 157
QY 85 AACATGCTGGAGCACTCTCTGATCCAGCCCGAAGATCCCATCCCTTCATGATCCAG 144
Db 158 AACATGCTGGAGCACTCTCTGATCCAGCCCGAAGATCCCATCCCTTCATGATCCAG 217
QY 145 CACTTGCATAGAGCAACGACAATGTGCCAGGATTGTAATATTAGGTCCACCCGCTCA 204
Db 218 CACTTGCATAGAGCAACGACAATGTGCCAGGATTGTAATATTAGGTCCACCCGCTCA 277
QY 205 GGGAAACAACTAGCAATGTGGCTCTGCAAAACATCTGAACAGAGTCTCTCCACCCCTG 264
Db 278 GGGAAACAACTAGCAATGTGGCTCTGCAAAACATCTGAACAGAGTCTCTCCACCCCTG 337
QY 265 GAGAACTGATCTTAATAGTTTCTCTATACGGCCACCGAGCCGAGGCTTTATCTG 324
Db 338 GAGAACTGATCTTAATAGTTTCTCTATACGGCCACCGAGCCGAGGCTTTATCTG 397
QY 325 CAAGGAAGACAGTTCACAGCGCGTCTGTCAGTGATTCAGGAAAGCTGCTGAA 384
Db 398 CAAGGAAGACAGTTCACAGCGCGTCTGTCAGTGATTCAGGAAAGCTGCTGAA 457
QY 385 GAGGATTGCATCAAGCAGGCTGGATTCCTGGATGGCATCCCTGAGACCGGTGAGCGCT 444
Db 458 GAGGATTGCATCAAGCAGGCTGGATTCCTGGATGGCATCCCTGAGACCGGTGAGCGCT 517
QY 445 CTGAGGATCCAGACCTGGGATCACACCCAGACAGTCTATGCTGCTGAGTCTCCAGAC 504
Db 518 CTGAGGATCCAGACCTGGGATCACACCCAGACAGTCTATGCTGCTGCTCCAGAC 577
QY 505 ACGTCTCTGATCGAGAGAACTTGGGAGAGATCGACCTCAAACTGGAGAGATTAT 564
Db 578 ACGTCTCTGATCGAGAGAACTTGGGAGAGATCGACCTCAAACTGGAGAGATTAT 637
QY 565 CACACACCTTTGATCGCCACCGAATCTGAATCCAGAACCGTCTCATGGTCCAGAG 624
Db 638 CACACACCTTTGATCGCCACCGAATCTGAATCCAGAACCGTCTCATGGTCCAGAG 697
QY 625 GACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTGGAGATTCATAGGAACATCGTCAGG 684
Db 698 GACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTGGAGATTCATAGGAACATCGTCAGG 757
QY 685 GTCAATTCCTCTCCCTCCCAAAATCTCAAGTCATCAGTCTGACCCAGCATGTGGAC 744
Db 758 GTCAATTCCTCTCCCTCCCAAAATCTCAAGTCATCAGTCTGACCCAGCATGTGGAC 817
QY 745 GTCTTCTACAGGCTCTGACCTATGTCCAAAGAAACCAATCGTACTAATGCCCGCTCAC 804
Db 818 GTCTTCTACAGGCTCTGACCTATGTCCAAAGAAACCAATCGTACTAATGCCCGCTCAC 877

QY 805 CCGAGGGTGTCTGCTCGGCTGTGGGAGTGGGAAAAGTCTGAGCCCGCCCTCTG 864
DB 878 CCGAGGGTGTCTGCTCGGCTGTGGGAGTGGGAAAAGTCTGAGCCCGCCCTCTG 937
QY 865 GCCAGAAATACAGGCTGTCAATGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA 924
DB 938 GCCAGAAATACAGGCTGTCAATGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA 997
QY 925 GATAGGACCAAGTGTGGGAGCTCATCCAGCCCTCTTTGAAAGAGAGTGGCAGTCTCT 984
DB 998 GATAGGACCAAGTGTGGGAGCTCATCCAGCCCTCTTTGAAAGAGAGTGGCAGTCTCT 1057
QY 985 GACAGCTCTCATGAAAGTGTGAGCCAGGCTGTGAGCAGGAGTGCATCCAGAAA 1044
DB 1058 GACAGCTCTCATGAAAGTGTGAGCCAGGCTGTGAGCAGGAGTGCATCCAGAAA 1117
QY 1045 GGCTGGGTGTCTACAGCGCTCCCGGGGACTCTGACAGGCAACCTGTGAAACCGCTG 1104
DB 1118 GGCTGGGTGTCTACAGCGCTCCCGGGGACTCTGACAGGCAACCTGTGAAACCGCTG 1177
QY 1105 GGCTACAAATCCAAACAGGCTGTGAAAGTGTGAGCAGGCTGTGAGCAGG 1164
DB 1178 GGCTACAAATCCAAACAGGCTGTGAAAGTGTGAGCAGGCTGTGAGCAGG 1237
QY 1165 CTGACTCTGAGAGAAATGATCCAGTCACTGGGAAAGGTACCACTCATGTGAAAGCCCA 1224
DB 1238 CTGACTCTGAGAGAAATGATCCAGTCACTGGGAAAGGTACCACTCATGTGAAAGCCCA 1297
QY 1225 CCTCCACCATGGAGATCAGGCTCGCTCTGAGAACCCAAAGGATGCTGAAAGCAG 1284
DB 1298 CCTCCACCATGGAGATCAGGCTCGCTCTGAGAACCCAAAGGATGCTGAAAGCAG 1357
QY 1285 GTCAAGCTGAAATGAGCTGTCTACAGGAATCAGCTGACTTGGAGCAGTTGTATGGG 1344
DB 1358 GTCAAGCTGAAATGAGCTGTCTACAGGAATCAGCTGACTTGGAGCAGTTGTATGGG 1417
QY 1345 TCGGCAATCACTCAATGGGACCCAGGACCCATACACAGTCTTCGAATACATCGAGT 1404
DB 1418 TCGGCAATCACTCAATGGGACCCAGGACCCATACACAGTCTTCGAATACATCGAGT 1477
QY 1405 GGGATCAATTAATCCCTGCGCCAGAAATCCCTGA 1440
DB 1478 GGGATCAATTAATCCCTGCGCCAGAAATCCCTGA 1513

RESULT 5
ADB63503
ID ADB63503 standard; cDNA; 1619 BP.
XX
AC ADB63503;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone TBS2120244460.
XX
KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW tissue regeneration; cell regeneration; membrane protein;
KW signal transduction-related protein; transcription-related protein;
KW osteoporosis; neurological disease; cancer; tumour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 684..1511
FT /*tag= a
FT /product= "Clone TBS2120244460 protein"
XX
PN EF1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.

XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
PI Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR P-PSDB; ADB65473.
XX
DR New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC proteins may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.
XX
SQ Sequence 1619 BP; 397 A; 469 C; 425 G; 328 T; 0 U; 0 Other;

Query Match 81.2%; Score 1170; DB 10; Length 1619;
Best Local Similarity 93.3%; Pred. No. 1.4e-294;
Matches 1272; Conservative 0; Mismatches 0; Indels 92; Gaps 1;
QY 169 GTGCCAGGATTGTAATATTAGTCCACCGGCTCAGGGAAAACAAATAGCAATGTGG 228
DB 148 GTGCCAGGATTGTAATATTAGTCCACCGGCTCAGGGAAAACAAATAGCAATGTGG 207
QY 229 CTCTGCAAAATCTGAAACAGCAGTCTCTCACCTCGAGAACCTGATCTTAATGAGTTT 288
DB 208 CTCTGCAAAATCTGAAACAGCAGTCTCTCACCTCGAGAACCTGATCTTAATGAGTTT 267
QY 289 TCCTATACGGCCACCGAGGCAAGGCTTTATCTGCAAGGAGGACAGTCTCCAGCGCG 348
DB 268 TCCTATACGGCCACCGAGGCAAGGCTTTATCTGCAAGGAGGACAGTCTCCAGCGCG 327
QY 349 CTGCTCTCCAGCTGATTCAGGAACCGCTGGCTGAGAGGATTCATCAGCAG----- 402
DB 328 CTGCTCTCCAGCTGATTCAGGAACCGCTGGCTGAGAGGATTCATCAGCAGTTGGAA 387
QY 403 ----- 402
DB 388 GTTTCCTGTAATAGCCCGCTTCGAGTTTTCATCGGCTAATTCAGTATCTGAGTTACGTG 447
QY 403 -----GGCTGGATTCCTGGATGGCATCCCTGAGACGGCTG 436
DB 448 GTGGTGACATCTGTATCTGCTCTCATGCTGGATTCCTGGATGGCATCCCTGAGACGGCTG 507

PT	treating, preventing and diagnosing pathological conditions with NOVX-
PT	associated disorders, such as cancer, obesity, diabetes and inflammatory
PT	or CNS diseases.
XX	Claim 20; SEQ ID NO 127; 772pp; English.
XX	The invention relates to novel isolated polypeptides, mature form of the
CC	polypeptide, a sequence that is 95% identical to the polypeptide or the
CC	polypeptide comprising one or more conservative substitutions. The NOVX
CC	polypeptide is useful for treating or preventing a pathology associated
CC	with the polypeptide e.g. disorders associated with aberrant expression
CC	or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC	endocrine, CNS and inflammatory disorders. They can also be used in
CC	various detection and screening assays, chromosome mapping, tissue typing
CC	and predictive medicine. This sequence corresponds to the coding sequence
CC	for one of the polypeptides of the invention.
XX	Sequence 1967 BP; 461 A; 594 C; 555 G; 357 T; 0 U; 0 Other;
XX	Query Match 81.0%; Score 1166; DB 10; Length 1967;
XX	Best Local Similarity 90.8%; Pred. No. 1.7e-293;
XX	Matches 1308; Conservative 0; Mismatches 0; Indels 132; Gaps 1;
QY	1 ATGACGCGCACTATCGCCCGCAGCGGTATCCCCCGGAGATGCCCAAGTACGGGGAGGAG 60
DB	552 ATGGAGCGCACTATCGCCCGCAGCGGTATCCCCCGGAGATGCCCAAGTACGGGGAGGAG 611
QY	61 AACCACTCTTCGAGTTGATCGAGACATGCTGAGCAACTCTGATCCACGACCCGAA 120
DB	612 AACCACTCTTCGAGTTGATCGAGACATGCTGAGCAACTCTGATCCACGACCCGAA 671
QY	121 GATCCATCCCTTCCATGATCAGACATCTTGATAGAGACAAAGCAATGTGCCAGGATT 180
DB	672 GATCCATCCCTTCCATGATCAGACATCTTGATAGAGACAAAGCAATGTGCCAGGATT 731
QY	181 GTAATATTAGTTCACCGCCCTCAGGAAACAAATAGCAATGTGGCTCGCAACAT 240
DB	732 GTAATATTAGTTCACCGCCCTCAGGAAACAAATAGCAATGTGGCTCGCAACAT 791
QY	241 CTGACAGCGAGTCTCTCACCCTGAGAACCTGATCTTAATAGATTTTCTATACGCCC 300
DB	792 CTGACAGCGAGTCTCTCACCCTGAGAACCTGATCTTAATAGATTTTCTATACGCCC 851
QY	301 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTTCCAGCGCGCTGCTCGTCCAG 360
DB	852 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTTCCAGCGCGCTGCTCGTCCAG 911
QY	361 CTGATTCAGAACGCTGCTGAGAGGATTCATCAAGCAGGGCTGATTTCTGGATGGC 420
DB	912 CTGATTCAGAACGCTGCTGAGAGGATTCATCAAGCAGGGCTGATTTCTGGATGGC 971
QY	421 ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTTGGGATCACACCCAGACAC 480
DB	972 ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACCTTGGGATCACACCCAGACAC 1031
QY	481 GTCAATGTGAGTCTCAGACAGCGTCTGATCGAGAACTTGGGGAAGAGATC 540
DB	1032 GTCAATGTGAGTCTCAGACAGCGTCTGATCGAGAACTTGGGGAAGAGATC 1091
QY	541 GACCCCTCAACTCGAGAGATTTATCACACACCTTTGACTGGCCACCCGAAATCTGAAATC 600
DB	1092 GACCCCTCAACTCGAGAGATTTATCACACACCTTTGACTGGCCACCCGAAATCTGAAATC 1151
QY	601 CAGAACCGTCTCATGTGTCAGAGGACATCTCAGAGCTGGAGCGGCTCAGAACTGCTG 660
DB	1152 CAGAACCGTCTCATGTGTCAGAGGACATCTCAGAGCTGGAGCGGCTCAGAACTGCTG 1211
QY	661 GAGTATCATAGGACATCTGTCAGGCTCATTTCCCTTACCCCAAAATCTCAAGTCATC 720
DB	1212 GAGTATCATAGGACATCTGTCAGGCTCATTTCCCTTACCCCAAAATCTCAAGTCATC 1271
QY	721 AGTGCTCAGCAGGATGTGTGGACGCTTCTTACAGGCTCTGACCTATGTCCAAAGCAAC 780

DB	1272 AGTGCTCAGCAGCAGCATGTGTGGAGCTTTCTACAGGCTCTGACCTATGTCCAAAGCAAC 1331
QY	781 CATCGTACTAATGCCCGTTTCACCCCGAGGGTGTCTGTCTGGGCGCTGTGGGAGTGGG 840
DB	1332 CATCGTACTAATGCCCGTTTCACCCCGAGGGTGTCTGTCTGGGCGCTGTGGGAGTGGG 1391
QY	841 AAAAGTCTGAGGGCGGCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTGTGTGGG 900
DB	1392 AAAAGTCTGAGGGCGGCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTGTGTGGG 1451
QY	901 CAACCTGCTGAAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 960
DB	1452 CAACCTG----- 1457
QY	961 TTTGAAAAGAGATGGCAGTTCTCTGACAGCCTCTCATGAAGTGTGTGAGCCAGGCGCTG 1020
DB	1458 ----- 1457
QY	1021 GACCAGCAGGACTGATCCAGAAAGGCTGGGTGTGTACACGGCGTCCCGGGGAGCTCGAC 1080
DB	1458 -----CAGAAAGGCTGGGTGTGTACACGGCGTCCCGGGGAGCTCGAC 1499
QY	1081 CAGGCACACCTGCTGAACCGCTGGGCTCAATCCCAACAGGGTGTCTTCTGTAATGTG 1140
DB	1500 CAGGCACACCTGCTGAACCGCTGGGCTCAATCCCAACAGGGTGTCTTCTGTAATGTG 1559
QY	1141 CAATTGTATTCATCATGAGGCGGCTGACTCTGAGAGAAATTTGATCCAGTCACTGGGAA 1200
DB	1560 CAATTGTATTCATCATGAGGCGGCTGACTCTGAGAGAAATTTGATCCAGTCACTGGGAA 1619
QY	1201 AGGTACACCTCATGTACAAAGCAGCTCCCAATGAGAGATCCAGGCTCGCTCTGTCAG 1260
DB	1620 AGGTACACCTCATGTACAAAGCAGCTCCCAATGAGAGATCCAGGCTCGCTCTGTCAG 1679
QY	1261 AACCCAAAGGATGCTGAAAGAGCAGTCAAGCTGAAATGAGCTTTCTACAGGAATCA 1320
DB	1680 AACCCAAAGGATGCTGAAAGAGCAGTCAAGCTGAAATGAGCTTTCTACAGGAATCA 1739
QY	1321 GCTGACTCTGGAGCAGTTGATGCTGGCCATCACTCAATGGGAGCAGGACCCATAC 1380
DB	1740 GCTGACTCTGGAGCAGTTGATGCTGGCCATCACTCAATGGGAGCAGGACCCATAC 1799
QY	1381 ACAGTCTTCTGAAATACATCAGAGTGGATCATTAATCCCTGCCCAAGAAATCCCTCA 1440
DB	1800 ACAGTCTTCTGAAATACATCAGAGTGGATCATTAATCCCTGCCCAAGAAATCCCTCA 1859

RESULT 7
AADI4324
ID AAD14324 standard; cdna; 1452 BP.

XX AC AAD14324;

XX DT 01-NOV-2001 (first entry)

XX XX Human 27802 adenylate kinase cdna.

Human; 27802 protein; adenylate kinase; cellular proliferative disorder;
neurological disorder; inflammatory disorder; lymphatic disorder;
cardiovascular disorder; respiratory disorder; haematological disorder;
Crohn's disease; atherosclerosis; pernicious anaemia; asthma; leukaemia;
acquired immune deficiency syndrome; AIDS; multiple sclerosis; lymphoma;
Alzheimer's disease; systemic lupus erythematosus; SLE; gene therapy;
lymphoblastic leukaemia; T-cell neoplasm; cytostatic; neuroprotective;
tissue typing; antileukemic; chromosomal mapping; nontropic;
dermatological; antiinflammatory; immunosuppressive; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX 219. .995
XX CDS /*tag= a
XX /product= "Human 27802 adenylate kinase"

```
FT misc_feature 219..992
FT /tag= b
FT /note= "This region is specifically referred in claim 2"
FT sig_peptide 219..386
FT /tag= b
FT mat_peptide 387..992
FT /tag= c
FT /product= "Human mature 27802 adenylate kinase"
XX WO200159082-A1.
XX 16-AUG-2001.
XX 12-FEB-2001; 2001WO-US004573.
XX 10-FEB-2000; 2000US-0181705P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Kapeller-Libermann R, Chun M;
XX WPI; 2001-514661/56.
XX P-PSDB; AAE07843.
XX
XX New adenylate kinase polypeptide for diagnosing/treating cellular
XX proliferative and/or differentiative, neurological, immune, inflammatory,
XX lymphatic, cardiovascular, respiratory and hematological disorders.
XX
XX Claim 2; Fig 1; 108pp; English.
XX
XX The present sequence is a cDNA encoding human 27802 adenylate kinase. The
XX 27802 protein and its corresponding nucleotide sequence is useful for
XX modulating diagnosing and treating cellular proliferative and/or
XX differentiative, neurological, inflammatory, lymphatic, cardiovascular,
XX immune, respiratory and hematological disorders. 27802 sequence is
XX useful for treating immune disorders (e.g., Crohn's disease), disorders
XX involving blood vessels (e.g., atherosclerosis), disorders involving red
XX cells (e.g., pernicious anemia), respiratory disorders (e.g., asthma),
XX deficiency syndrome (AIDS), multiple sclerosis, Alzheimer's disease),
XX disorders involving T-cells (e.g., systemic lupus erythematosus),
XX diseases involving haematopoietic stem cells (e.g., leukaemia), disorders
XX involving B-cells (e.g., lymphoblastic leukaemia/lymphoma) and disorders
XX modulating cellular growth and/or cellular metabolic pathways,
XX particularly for regulating one or more proteins involved in growth and
XX metabolism. 27802 DNA is used in gene therapy. 27802 sequence or its
XX antibody are useful in screening assays, detection assays (e.g.,
XX chromosomal mapping, tissue typing, forensic biology), preventive
XX medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
XX trials and pharmacogenomics) and in methods of treatment
XX
XX Sequence 1452 BP; 398 A; 414 C; 364 G; 276 T; 0 U; 0 Other;
XX
XX Query Match 71.7%; Score 1032.8; DB 4; Length 1452;
XX Best Local Similarity 86.5%; Pred. No. 8.3e-259;
XX Matches 1246; Conservative 0; Mismatches 2; Gaps 2;
XX
XX 1 ATGAGCGCACTATCGCCCGCACCGTATCCCGCCCGATGCCCGATCCCGATCCCGGAGGAG 60
XX 53 ATGAGCGCACTATCGCCCGCACCGTATCCCGCCCGATGCCCGATCCCGGAGGAG 112
XX
XX 61 AACCACTCTTCAGTTGATGCGAACAATGCTGAGGCACTCTCTGATCCACAGCCCGAA 120
XX 113 AACCACTCTTCAGTTGATGCGAACAATGCTGAGGCACTCTCTGATCCACAGCCCGAA 172
XX
XX 121 GATCCCATCCCTTCATGATCCAGCACTTGCATAGAGCAACGACAAATGTGCCAGGATT 180
XX 173 GATCCCATCCCTTCATGATCCAGCACTTGCATAGAGCAACGACAAATGTGCCAGGATT 221
XX
XX 181 GTAATATTAGTCTCCACCCGCTCAGGGAAACAACTAGCAATGCTCTGCAACAT 240
XX 222 -----GCATGTGGCTCTGCACAT 242
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Qy 241 CTGAACAGAGTCTCTCTCACCTGGAGAACCTGATCTTAAATGAGTTTTCTATACGGCC 300
Db 243 CTGAACAGAGTCTCTCTCACCTGGAGAACCTGATCTTAAATGAGTTTTCTATACGGCC 302
Qy 301 ACCGAAGCCAGAGGCTTTATCTGCAAGAGAGACAGTTCCAGCGGCTGCTCGTCCAG 360
Db 303 ACCGAAGCCAGAGGCTTTATCTGCAAGAGAGACAGTTCCAGTGGCTGCTCGTCCAG 362
Qy 361 CTGATTCTAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCTGATCTTGGATGGC 420
Db 363 CTGATTCTAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCTGATCTTGGATGGC 422
Qy 421 ATCCCTGAGAGCGCTGAGCAGGCTCTGAGGATCCAGACCTTGGGGATCAACCCAGACAC 480
Db 423 ATCCCTGAGAGCGCTGAGCAGGCTCTGAGGATCCAGACCTTGGGGATCAACCCAGACAC 482
Qy 481 GTCAATTGTGCTGCTCCAGACACGCTCTGATCGAGAGAAACTTTGGGGAAGAGAAATC 540
Db 483 GTCAATTGTGCTGCTCCAGACACGCTCTGATCGAGAGAAACTTTGGGGAAGAGAAATC 542
Qy 541 GACCCCTCAAACTGGAGAGATTTATCACACCACTTTGACTGGCCACCCGGAATCTGAAATC 600
Db 543 GACCCCTCAAACTGGAGAGATTTATCACACCACTTTGACTGGCCACCCGGAATCTGAAATC 602
Qy 601 CAGAACGCTCTCATGCTGTCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 660
Db 603 CAGAACGCTCTCATGCTGTCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 662
Qy 661 GAGTATCATAGGAACATGTCAGGCTCATTCCTCTTACCCCAAAATCTCTCAAGTCATC 720
Db 663 GAGTATCATAGGAACATGTCAGGCTCATTCCTCTTACCCCAAAATCTCTCAAGTCATC 722
Qy 721 AGTGTGACACGAGCATGTGTGGACGCTCTTACACAGGCTCTGACCTATGTGCAAAACAAC 780
Db 723 AGTGTGACACGAGCATGTGTGGACGCTCTTACACAGGCTCTGACCTATGTGCAAAACAAC 782
Qy 781 CATGCTACTTAATCCCGCTTACCCCGAGGCTGCTGCTCGGGCTGTTGGGCGATGGG 840
Db 783 CATGCTACTTAATCCCGCTTACCCCGAGGCTGCTGCTCGGGCTGTTGGGCGATGGG 842
Qy 841 AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATAAGGCTGTGCAATGTCTGTGTTGGG 900
Db 843 AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATAAGGCTGTGCAATGTCTGTGTTGGG 902
Qy 901 CAATGCTGAAAGAGGCTGTGCGAGATAGGACACAGCTTTGGCGAGCTCATTCAGGCCCTTC 960
Db 903 CAATGCTGAAAGAGGCTGTGCGAGATAGGACACAGCTTTGGCGAGCTCATTCAGGCCCTTC 962
Qy 961 TTTGAAAGAGGATGGCAGTTCTCTGACAGCCTCTCTCATGAAGTGTGTGAGCCAGCGCTG 1020
Db 963 TTTGAAAGAGGATGG- 978
Qy 1021 GACCAGCAGGACTGCATCCAGAAAGCTGGGTGTACACGCGCTCCCGCGGAGACCTCGAC 1080
Db 979 ----- 978
Qy 1081 CAGGCACACCTGCTGAAACCGCTGGGCTTACAATCCCAACAGGCTGTTTTCTCTGAATGTG 1140
Db 979 -----CAGGCTGTTTTTCTCTGAATGTG 1000
Qy 1141 CCATTTGATTTCCATCATGAGCGGCTGACTCTGAGAGAAATTTGATCAGTCACTCGGGAA 1200
Db 1001 CCATTTGATTTCCATCATGAGCGGCTGACTCTGAGAGAAATTTGATCAGTCACTCGGGAA 1060
Qy 1201 AGGTACCACTCATGTACAGCAACCTCCCAACATGAGATCCAGCTCGCTCTCTCGAG 1260
Db 1061 AGGTACCACTCATGTACAGCAACCTCCCAACATGAGATCCAGCTCGCTCTCTCGAG 1120
Qy 1261 AACCCAAAGATGCTGAAAGAGAGGCTCAGCTGAAATGGAATCTGTTCTTACAGGAATCA 1320
Db 1121 AACCCAAAGATGCTGAAAGAGAGGCTCAGCTGAAATGGAATCTGTTCTTACAGGAATCA 1180
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QY 1321 GCTGACTGGAGCAGTTGTATGGTGGCCCATCACCTCAATGGGACGAGGACCCATAC 1380
 DB 1181 GCTGACTGGAGCAGTTGTATGGTGGCCCATCACCTCAATGGGACGAGGACCCATAC 1240
 QY 1381 ACAGTCTCGAATACATCGAGAGTGGGATCAATATCCCTGCGCCCAAGAAATCCCTGA 1440
 DB 1241 ACAGTCTCGAATACATCGAGAGTGGGATCAATATCCCTGCGCCCAAGAAATCCCTGA 1300

RESULT 8

ID AAD61170 standard; cDNA; 1452 BP.

XX AAD61170;

XX 15-JAN-2004 (first entry)

XX Human 27802, adenylate kinase cDNA.

XX Human; ATPase-like protein; phosphatidylserine synthase-like protein;
 KW DNA fragmentation factor-like protein; vesicle-mediated transport;
 KW phospholipid scramblase-like protein; adenylate kinase protein;
 KW organelle biogenesis; cell-cycle regulation; primary brain lymphoma;
 KW protein degradation; splenomegaly; pulmonary embolism; Hodgkin disease;
 KW atresia; tuberculosis; astrocyte; apoptosis; neurodegenerative disease;
 KW DNA fragmentation; autoimmune disorder; cancer; blood clotting system;
 KW immune system; haematopoietic; hypertension; systemic sclerosis;
 KW atherosclerosis; leukopenia; oligodendrocyte; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 219..995

XX /*tag= a

XX /product= "Human 27802, adenylate kinase protein"

XX /*tag= b

XX /note= "This region is specifically claimed as SEQ ID NO:
 23 in claim 1 of the specification"

XX US2003092116-A1.

XX 15-MAY-2003.

XX 07-JUN-2002; 2002US-00165800.

XX 10-FEB-2000; 2000US-0181705P.

XX 29-FEB-2000; 2000US-0185609P.

XX 29-FEB-2000; 2000US-0185946P.

XX 29-FEB-2000; 2000US-0185947P.

XX 12-FEB-2001; 2001US-00781677.

XX 21-FEB-2001; 2001US-00790179.

XX 21-FEB-2001; 2001US-00790180.

XX 22-FEB-2001; 2001US-00790838.

XX 26-FEB-2001; 2001US-00795038.

XX (MILL-) MILLENNIUM PHARM INC.

XX Chun M, Gluckmann MA, Kapeller-Libermann R, Meyers RE;

XX WPI; 2003-765479/72.

XX P-P8DB; ABW00581.

XX New isolated polypeptides including phosphatidylserine synthase-like
 PT polypeptide useful for identifying a compound which binds and modulates
 PT activity of the polypeptide useful for treating diseases, e.g. cancer.

XX Claim 1; Fig 28; Opp; English.

XX The present invention relates to novel proteins including ATPase-like
 CC proteins, phosphatidylserine synthase-like proteins, DNA fragmentation
 CC factor-like proteins, phospholipid scramblase-like proteins or adenylate

CC kinase proteins and polynucleotides encoding such proteins. The human
 CC ATPase-like molecules are useful for modulating ATPase function. They are
 CC useful in modulating organelle biogenesis, cell-cycle regulation, protein
 CC degradation and vesicle-mediated transport. They are also useful for
 CC treating disorders associated with aberrant ATPase-like expression or
 CC activity such as splenomegaly, pulmonary embolism, atresia and primary
 CC brain lymphoma. The human phosphatidylserine synthase-like molecules are
 CC useful for modulating the biosynthetic pathway involving the synthesis of
 CC the membrane phosphatidylserine (PS). They human phosphatidylserine
 CC synthase-like molecules are useful for treating disorders associated with
 CC aberrant human phosphatidylserine synthase activity such as tuberculosis,
 CC astrocytes and Hodgkin disease. The human 5698, DNA fragmentation factor-
 CC like molecules are useful for modulating apoptotic events, including DNA
 CC fragmentation. The human 5698 molecules are useful for treating diseases
 CC such as autoimmune disorders, neurodegenerative diseases and cancer. The
 CC human 32621, phospholipid scramblase-like molecules are useful for
 CC modulating immune, haematopoietic and blood clotting systems. They are
 CC useful for treating a disorder associated with aberrant human
 CC phospholipid scramblase-like protein activity such as leukopenia and
 CC systemic sclerosis. The human 27802 adenylate kinase are useful for
 CC modulating cellular growth and/or cellular metabolic pathways. They are
 CC useful for treating hypertension, atherosclerosis and oligodendrocytes.
 CC The present sequence is human 27802, adenylate kinase cDNA

XX Sequence 1452 BP; 398 A; 414 C; 364 G; 276 T; 0 U; 0 Other;

XX Query Match 71.7%; Score 1032.8; DB 10; Length 1452;

XX Best Local Similarity 86.5%; Pred. No. 8.3e-259; Indels 192; Gaps 2;
 XX Matches 1246; Conservative 0; Mismatches 2;

QY 1 ATGGAGCGCCACTATCGCCCGCACCGTATCCCGCCGAGATCCCCAGTACGGGGAGGAG 60
 DB 53 ATGGAGCGCCACTATCGCCCGCACCGTATCCCGCCGAGATCCCCAGTACGGGGAGGAG 112
 QY 61 AACCAACATCTTCGAGTTGATGAGCAACATGCTGGAGCAACTCTCTGATCACCAGCCGAA 120
 DB 113 AACCAACATCTTCGAGTTGATGAGCAACATGCTGGAGCAACTCTCTGATCACCAGCCGAA 172
 QY 121 GATCCCATCCCTTCATGATCCAGCACTTCATAGAGACAACACAAATGTGCCAGGATT 180
 DB 173 GATCCCATCCCTTCATGATCCAGCACTTCATAGAGACAACACAAATGTGCCAGGATT 221
 QY 181 GTAATATTAGTCCACCGCCTCAGGGAAAAACAATAGCAATGTGGCTCTGCAAAACAT 240
 DB 222 -----GCAATGTGGCTCTGCAAAACAT 242

QY 241 CTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATAGATTTTCTCTATACGGCC 300

DB 243 CTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATAGATTTTCTCTATACGGCC 302

QY 301 ACCGAAGCCAGAGAGGCTTTTATCTGCAAAAGGAAGACAGATTTCCACGCGCTGCTCCAG 360

DB 303 ACCGAAGCCAGAGAGGCTTTTATCTGCAAAAGGAAGACAGATTTCCACGCGCTGCTCCAG 362

QY 361 CTGATTCAGGAACCGCTGGCTGAAGAGGATTGATCAAGCAGGGCTGGATTCTGGATGGC 420

DB 363 CTGATTCAGGAACCGCTGGCTGAAGAGGATTGATCAAGCAGGGCTGGATTCTGGATGGC 422

QY 421 ATCCCTGAGAGCGGTGAGCAGGCTCTGAGGATCCAGACCTCGGGGATCACCCACAGACAC 480

DB 423 ATCCCTGAGAGCGGTGAGCAGGCTCTGAGGATCCAGACCTCGGGGATCACCCACAGACAC 482

QY 481 GTCAATTGTCTGAGTGTCTCCAGACACGGTCTCTGATCCAGAGAAATTTGGGGAGAGAAATC 540

DB 483 GTCAATTGTCTGAGTGTCTCCAGACACGGTCTCTGATCCAGAGAAATTTGGGGAGAGAAATC 542

QY 541 GACCTTCAAACTGAGAGATTATCACACCACTTTGACCTGGCCACCCCGAATCTGAAATC 600

DB 543 GACCTTCAAACTGAGAGATTATCACACCACTTTGACCTGGCCACCCCGAATCTGAAATC 602

QY 601 CAGAACCGTCTCATGTGTGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTG 660

DB 603 CAGAACCGTCTCATGTGTGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAACTGCTG 662

QY 661 GAGTATCATAGGAACATCGTCAGGGTCATTCCTCTACCCCAAAATCCTCAAAGTCATC 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 663 GAGTATCATAGGAACATCGTCAGGGTCATTCCTCTACCCCAAAATCCTCAAAGTCATC 722
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 721 AGTGTGACACGACCATGTGTGACGCTCTTCTACAGGCTCTGACCTATGTCCAAAGCAAC 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 723 AGTGTGACACGACCATGTGTGACGCTCTTCTACAGGCTCTGACCTATGTCCAAAGCAAC 782
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 781 CATCGTACTAATGCCCCGCTTACCCGAGGGTCTCTCTCGGGCCCTGTGGGCACTGGG 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 783 CATCGTACTAATGCCCCGCTTACCCGAGGGTCTCTCTCGGGCCCTGTGGGCACTGGG 842
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 841 AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTCTGGG 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 843 AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTCTGGG 902
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 901 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCAAGTTTGGCGAGCTCATCCAGCCCTTC 960
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 903 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCAAGTTTGGCGAGCTCATCCAGCCCTTC 962
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 961 TTTGAAAGAGGATGGCAGTTCTCTGACAGCTCTCTCATGAAGGTCTGAGCCAGCCCTG 1020
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 963 TTTGAAAGAGGATGG ----- 978
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1021 GACCAGCAGGACTGCATCCAGAAAGGCTGGGTGCTACAGGCGTCCCGCGGAGCTCGAC 1080
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 979 ----- 978
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1081 CAGGCACACCTGCTGAACCGCTGGGCTACAAATCCCAACAGGGTGTCTTCTGAAATGG 1140
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 979 -----CAGGGTGTCTTCTGAAATGG 1000
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1141 CCAATTGATTCATCATGAGCGGCTGACTCTGAGAAGAAATGATCCAGTCACTGGGGA 1200
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1001 CCAATTGATTCATCATGAGCGGCTGACTCTGAGAAGAAATGATCCAGTCACTGGGGA 1060
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1201 AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCGAGGCTGCGCTCTGCGAG 1260
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1061 AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCGAGGCTGCGCTCTGCGAG 1120
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QY 1261 AACCAAGAGTGTGAAAGCAGCGTCAAGCTGGAATGACCTGTCTACAGGAATCA 1320
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1121 AACCAAGAGTGTGAAAGCAGCGTCAAGCTGGAATGACCTGTCTACAGGAATCA 1180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1321 GCTGACTTGAGCAGTTGTATGGGTGCGCCATCACTCAATGGGACGAGCAGCCATAC 1380
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1181 GCTGACTTGAGCAGTTGTATGGGTGCGCCATCACTCAATGGGACGAGCAGCCATAC 1240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1381 ACAGTCTTCGAATACATCGAGTGGGATCAATCCCTGCGCCAGGAATCCCTGA 1440
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1241 ACAGTCTTCGAATACATCGAGTGGGATCAATCCCTGCGCCAGGAATCCCTGA 1300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9

ID AAS27222 standard; cdna; 1223 BP.

AC AAS27222;

XX 07-NOV-2001 (first entry)

DE cdna encoding novel signal transduction pathway protein, Seq ID 257.

XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS; ss;

acquired immune deficiency syndrome.

Homo sapiens.

WO200154733-A1.

02-AUG-2001.

17-JAN-2001; 2001WO-US001312.

31-JAN-2000; 2000US-0179065P.

04-FEB-2000; 2000US-0180628P.

24-FEB-2000; 2000US-0184664P.

02-MAR-2000; 2000US-0186350P.

16-MAR-2000; 2000US-0189874P.

17-MAR-2000; 2000US-0190076P.

18-APR-2000; 2000US-0198123P.

19-MAY-2000; 2000US-0205515P.

07-JUN-2000; 2000US-0209467P.

28-JUN-2000; 2000US-0214886P.

30-JUN-2000; 2000US-0215135P.

07-JUL-2000; 2000US-0216647P.

07-JUL-2000; 2000US-0216880P.

11-JUL-2000; 2000US-0217487P.

11-JUL-2000; 2000US-0217496P.

14-JUL-2000; 2000US-0218290P.

26-JUL-2000; 2000US-0220963P.

26-JUL-2000; 2000US-0220964P.

14-AUG-2000; 2000US-0224518P.

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14-AUG-2000; 2000US-0225213P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225266P.

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18-AUG-2000; 2000US-0226279P.

22-AUG-2000; 2000US-0226681P.

22-AUG-2000; 2000US-0226868P.

22-AUG-2000; 2000US-0227182P.

23-AUG-2000; 2000US-0227009P.

01-SEP-2000; 2000US-0228924P.

01-SEP-2000; 2000US-0229343P.

01-SEP-2000; 2000US-0229344P.

05-SEP-2000; 2000US-0229345P.

05-SEP-2000; 2000US-0229509P.

06-SEP-2000; 2000US-0229513P.

06-SEP-2000; 2000US-0230437P.

08-SEP-2000; 2000US-0230438P.

08-SEP-2000; 2000US-0231242P.

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08-SEP-2000; 2000US-0231244P.

08-SEP-2000; 2000US-0231413P.

08-SEP-2000; 2000US-0231414P.

08-SEP-2000; 2000US-0232080P.

12-SEP-2000; 2000US-0231968P.

14-SEP-2000; 2000US-0232397P.

14-SEP-2000; 2000US-0232398P.

14-SEP-2000; 2000US-0232399P.

14-SEP-2000; 2000US-0232400P.

14-SEP-2000; 2000US-0232401P.

14-SEP-2000; 2000US-0233063P.

14-SEP-2000; 2000US-0233064P.

14-SEP-2000; 2000US-0233065P.

21-SEP-2000; 2000US-0234223P.

21-SEP-2000; 2000US-0234274P.

25-SEP-2000; 2000US-0234977P.

Mon Mar 21 09:11:05 2005

PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
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PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
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PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 17-NOV-2000; 2000US-0249301P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX P-PSDB; AAU17305.
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX PT prognosing disorders related to the proteins, including cancers, immune
XX PT disorders and neuronal disorders.
XX Claim 1; SEQ ID NO 257; 880pp; English.
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
XX diagnosing, preventing and treating diseases including immune system
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
XX transplant rejections and graft versus host disease, infectious diseases
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
XX other blood-related disorders (sickle cell anaemia), myeloproliferative
XX disorders, primary haematopoietic disorders, hyperproliferative disorders
XX (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
XX Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
XX (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
XX glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
XX respiratory disorders, dermatological disorders, in wound healing,
XX epithelial cell proliferation, endocrine disorders (e.g. Addison's
XX disease), reproductive system disorders, gastrointestinal disorder
XX (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
XX B-cell responsiveness to pathogens, activators of T-cells, to induce
XX higher affinity antibodies, and as a means to induce tumour proliferation
XX in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
XX AAS27850 represent novel signal transduction pathway protein coding
XX sequences and PCR primers of the invention

Query Match 71.4%; Score 1027.6; DB 4; Length 1223;
Best Local Similarity 95.6%; Pred. No. 1.8e-257;
Matches 1153; Conservative 0; Mismatches 10; Indels 43; Gaps 8;
QY 1 ATGGAGCCACTATCGCCCGCAGCCGATATCCCGCCGAGATCCCGAGTACGGGAGGAG 60
DB 6 ATGACGCCACTATCGCCCGCAGCCGATATCCCGCCGAGATCCCGAGTACGGGAGGAG 63
QY 61 AACCATCTTCGATTGATG-----CAG 84
DB 64 AACCATCTTCGATTGATGATTAACCACTGGGTGTCTGCCCTGCACCCACAG 123
QY 85 AACATGCTGGAGCAACTCTCTGATCCACCGAGCCGAGATCCCATCCCTTCATGATCCAG 144
DB 124 AACATGCTGGAGCAACTCTCTGATCCACCGAGCCGAGATCCCATCCCTTCATGATCCAG 183
QY 145 CACTTGCATAGACAAACGCAATGTCGCCAGATGTTATATAGTCCACCGGCTCA 204
DB 184 CACTTGCATAGACAAACGCAATGTCGCCAGATGTTATATAGTCCACCGGCTCA 243
QY 205 GGGAAACCAATAGCAATGTCGCTCTGCAACATCTG-AAACAGAGTCTCTCTCAACCT 263
DB 244 GGGAAACCAATAGCAATGTCGCTCTGCAACATCTGCAACATCTGCAACAGAGTCTCTCAACCT 303
QY 264 GGA-GAACCTGATCTTAAATGAGTTTCTTATAGGCGCACCGAGCCAG-AAGGCTTTAT 321
DB 304 GGANGAACCTGATCTTAAATGAGTTTCTTATAGGCGCACCGAGCCAGAAAGGCTTTAT 363
QY 322 CTGCAAAAGGAGACAGTTCACCGGCGCTGCTCGTCAGCTGATTTCAGGAACCGCTGGCT 381
DB 364 CTGCAAAAGGAGACAGTTCACCGGCGCTGCTCGTCAGCTGATTTCAGGAACCGCTGGCT 423
QY 382 GAAGAGGATTGCATCAAGCAGGGGCTGGATTCTGGATGGCATTCCTGAGACGGGTGAGCAG 441
DB 424 GAAGAGGATTGCATCAAGCAGGGGCTGGATTCTGGATGGCATTCCTGAGACGGGTGAGCAG 482

QY 442 GCTCTGAGGATCCAGACCTGGGATCACACCCAGACAGTCAATGTGCTGAGTGCTCCA 501
DB 483 GCTCTGAGGATCCAGACCTGGGATCACACCCAGACAGTCAATGTGCTGAGTGCTCCA 542
QY 502 GACACCGTCTGATCGAGAGAACTTGGGGAAGAGATGACCCCTCAAACTGGAGAGATT 561
DB 543 GACACCGTCTGATCGAGAGAACTTGGGGAAGAGATGACCCCTCAAACTGGAGAGATT 602
QY 562 TATCACACACCTTTGATCGGCCACCCGAATCGAAATCGAAACCGTCTCATGGTGCCA 621
DB 603 TATCACACACCTTTGATCGGCCACCCGAATCGAAATCGAAACCGTCTCATGGTGCCA 662
QY 622 GAGGACATCTCAGAGCTGGAGACGGCTCAGAACTCTGGAGTATCATAGAACATCGTC 681
DB 663 GAGGACATCTCAGAGCTGGAGACGGCTCAGAACTCTGGAGTATCATAGAACATCGTC 722
QY 682 AGGGTCATTCCTCTACCCCAAAATCTCAAGTCATCAGTGTGACCGACCATGTGTG 741
DB 723 AGGGTCATTCCTCTACCCCAAAATCTCAAGTCATCAGTGTGACCGACCATGTGTG 782
QY 742 GAGCTCTTCTACCGGCTCTGACCTATGTCCAAAGCAACATCGTACTAATGCCCGTTC 801
DB 783 GAGCTCTTCTACCGGCTCTGACCTATGTCCAAAGCAACATCGTACTAATGCCCGTTC 842
QY 802 ACCCGAGGGTGTGCTGCTCGGGCTGTGGGCAAGTGGGAAAAAGTCTGCAGGCGGCCCTC 861
DB 843 ACCCGAGGGTGTGCTGCTCGGGCTGTGGGCAAGTGGGAAAAAGTCTGCAGGCGGCCCTC 902
QY 862 CTGGCCAGAAATACAGCTTGTCAATGTCTGCTGGGCACTGCTGAAGAGGCTGTG 921
DB 903 CTGGCCAGAAATACAGCTTGTCAATGTCTGCTGGGCACTGCTGAAGAGGCTGTG 962
QY 922 GCAGATAGGACCGCTTGGCGAGCTCATCAGCCCTCTTTGAAAAGAGATGGCAGTT 981
DB 963 GCAGATAGGACCGCTTGGCGAGCTCATCAGCCCTCTTTGAAAAGAGATGGCAGTT 1022
QY 982 CTGACAGCTCTCTATGAAAGGTGTGACCGACCGCTGGACAGCAGACTGCATCCAG 1041
DB 1023 CTGACAGCTCTCTATGAAAGGTGTGACCGACCGCTGGACAGCAGACTGCATCCAG 1082
QY 1042 AAAGCTGGGTGTGTACACGGCTCCCGGGGACCTCGACAGGCAACCTGCTGAACCGC 1101
DB 1083 AAAGCTGGGTGTGTACACGGCTCCCGGGGACCTCGACAGGCAACCTGCTGAACCGC 1142
QY 1102 CTGGGTACAA-TCCCAACAGGTGTGTTTCTGAAATGTCCTGATTCATCATGGA 1160
DB 1143 CTGGGTACAA-TCCCAACAGGTGTGTTTCTGAAATGTCCTGATTCATCATGGA 1202
QY 1161 CGGGCT 1166
DB 1203 NCGGT 1208

RESULT 10
ADB93400

ID ADB93400 standard; cDNA; 1223 BP.

XX AC ADB93400;

XX DT 04-DEC-2003 (first entry)

XX DE Human cDNA encoding a novel protein #247.

XX KW ss; gene; human; autoimmune disease; Parkinson's disease; silicosis;
XX KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
XX KW immunosuppressive agent; adjuvant; enhance immune response;
XX KW higher affinity antibody induction;
XX KW increased serum immunoglobulin concentration.

OS Homo sapiens.

XX US2002168711-A1.

XX PD 14-NOV-2002.
XX PF 17-JAN-2001; 2001US-00764868.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217486P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 08-SEP-2000; 2000US-0229513P.
PR 21-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 20-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 01-NOV-2000; 2000US-0241809P.
PR 17-NOV-2000; 2000US-0244617P.
PR 08-DEC-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-719985/68.
XX P-PSDB; ADB94013.
XX New isolated polypeptide useful for diagnosing and treating
XX immunosuppressive conditions such as autoimmune disease and Parkinson's
XX disease.
XX Claim 3; SEQ ID NO 257; 345pp; English.
XX The invention relates to an isolated polypeptide. The polypeptide is
XX useful for diagnosing a pathological condition or a susceptibility to a

CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in the nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents cDNA encoding a novel human protein. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format direct from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020168711.
XX
SQ Sequence 1223 BP; 305 A; 355 C; 310 G; 245 T; 0 U; 8 Other;

Query Match 71.4%; Score 1027.6; DB 10; Length 1223;
Best Local Similarity 95.6%; Pred. NO. 1.8e-257;
Matches 1153; Conservative 0; Mismatches 10; Indels 43; Gaps 8;
1 ATGGAGCCATATCGCCCGCCAGCGTATCCCGCCAGATGCCCGCAGTACCGGAGGAG 60
6 ATGGAGCCGACATATCGCCCGCCAGCGTATCCCGCCAGATGCCCGCAGTACCGGAGGAG 63
61 AACACATCTTCGAGTTGATG-----CAG 84
64 AACACATCTTCGAGTTGATGAGTATTAACACCTGGGTGTCTGCCCTGCACCCACAG 123
85 AACATCTGGAGCACTCTGATCCAGCCAGCCGAGATCCATCCCTTCATGATCCAG 144
124 AACATCTGGAGCACTCTGATCCAGCCAGCCGAGATCCATCCCTTCATGATCCAG 183
145 CACTTGCATAGAGACAACGACATATGCGCCAGATTTGTAATATTAGGTCCACCGCTCA 204
184 CACTTGCATAGAGACAACGACATATGCGCCAGATTTGTAATATTAGGTCCACCGCTCA 243
205 GGGAAACAAACATAGCAATGTGGCTCTGCAAAACATCTG-AACAGCATCTCCACCCCT 263
244 GGGAAACAAACATAGCAATGTGGCTCTGCAAAACATCTGAAACAGCATCTCCCTCACCCCT 303
264 GGA-CAACCTGATCTTAATAGTATTTCTTATACCGCCACCGAAGCCAG-AAGGCTTTAT 321
304 GGAGAAACCTGATCTTAATAGTATTTCTTATACCGCCACCGAAGCCAGAAAGCTTTAT 363
322 CTCGAAAGGAAGACAGTCTCCAGCGCGTCTGCTGCTCAAGTATTCAGGAACCGCTGCT 381
364 CTCGAAAGGAAGACAGTCTCCAGCGCGTCTGCTGCTCAAGTATTCAGGAACCGCTGCT 423
382 GAAGAGATGTCATCAAGCAGCGGTGATTTCTGATGGCATCCCTGAGACGGTGCAGCAG 441
424 GAAGAGATGTCATCAAGCAGCGGTGATTTCTGATGGCATCCCTGAGACGGTGCAGCAG 482
442 GCTCTGAGGATCCAGACCCCTGGGGATCACACCCAGACAGTCAATTGTGTGATGCTCA 501
483 GCTCTGAGGATCCAGACCCCTGGGGATCACACCCAGACAGTCAATTGTGTGATGCTCA 542
502 GACACGGTCTGATCGAGAGAACTTGGGAGAGAGATCGACCTCAACCTGAGAGATT 561
543 GACACGGTCTGATCGAGAGAACTTGGGAGAGAGATCGACCTCAACCTGAGAGATT 602

QY 562 TATCACCACCTTTGACTGGCCACCGAATCTGAATCCAGAACCGTCTCATGGTGCCA 621
DB 603 TATCACCACCTTTGACTGGCCACCGAATCTGAATCCAGAACCGTCTCATGGTGCCA 662
QY 622 GAGGACATCTCAGAGCTGGAGACGGCTCAGAAAATGCTGGAGTATCATAGGAACATCGT 681
DB 663 GAGGACATCTCAGAGCTGGAGACGGCTCAGAAAATGCTGGAGTATCATAGGAACATCGT 722
QY 682 AGGGTCATTCCCTCTACCCCAAAATCTCAAAGTCATCAGTGTGACGACGATGTG 741
DB 723 AGGGTCATTCCCTCTACCCCAAAATCTCAAAGTCATCAGTGTGACGACGATGTG 782
QY 742 GACGTCATTACCAAGCTCTGACCTATGTCCAAAGCAACCATCTGTAATGCCCCCTTC 801
DB 783 GACGTCATTACCAAGCTCTGACCTATGTCCAAAGCAACCATCTGTAATGCCCCCTTC 842
QY 802 ACCCCGAGGGTCTCTGCTCGGGCTGTGGGCTGTGGGCAAGTGTGACGACGCGCCCTC 861
DB 843 ACCCCGAGGGTCTCTGCTCGGGCTGTGGGCTGTGGGCAAGTGTGACGACGCGCCCTC 902
QY 862 CTGGCCCAAAATCAGAGCTTGTCAATGCTGTGCTGGGCAACTGCTGAAAAGAGGCTGTG 921
DB 903 CTGGCCCAAAATCAGAGCTTGTCAATGCTGTGCTGGGCAACTGCTGAAAAGAGGCTGTG 962
QY 922 GCAGATAGGACCACTGTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGAGATGCGATT 981
DB 963 GCAGATAGGACCACTGTTGGCGAGCTCATCCAGCCCTTCTTTGAAAAGAGATGCGATT 1022
QY 982 CTGACAGCCTCTCATGAAGTGTGACGACGCGCTGGACGACGACGATGATCCAG 1041
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QY 1102 CTGGGCTACAA-TCCCAACAGGGTGTGTTTCTGTAATGTCATTTGATTCATATGGA 1160
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QY 1161 GCGGCT 1166
DB 1203 NCGGCT 1208
RESULT 11
AAD26472
ID AAD26472 standard; cDNA; 995 BP.
XX
AC AAD26472;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human kinase PKIN-25 cDNA.
XX
KW Human; kinase; PKIN-25; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
CDS 43..870
FT /*tag= a
FT /product= "Human PKIN-25 protein"

XX WO200196547-A2.
 XX 20-DEC-2001.
 XX 14-JUN-2001; 2001WO-US019444.
 XX 15-JUN-2000; 2000US-0212073P.
 XX 23-JUN-2000; 2000US-0213467P.
 XX 30-JUN-2000; 2000US-0215651P.
 XX 07-JUL-2000; 2000US-0216605P.
 XX 13-JUL-2000; 2000US-0218372P.
 XX 25-AUG-2000; 2000US-0228056P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
 PI Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DM, Greenwald SR;
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YI;
 PI Paughn MB, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
 PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
 XX WPI; 2002-090207/12.
 DR P-PSDB; AAE16279.
 XX New polypeptides, useful for diagnosing, treating or preventing disorders
 of growth and development, cardiovascular and lipid, and diseases such as
 cancer, comprise human kinase polypeptides.
 XX Claim 5; Page 196; 197pp; English.
 XX The invention relates to human kinase PKIN proteins and their
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for
 CC treating a disease or condition associated with decreased expression of
 CC PKIN and a composition comprising PKIN antagonist is useful for treating
 CC a disease or condition associated with overexpression of PKIN. The
 CC disorders include cancer (leukemia, adenocarcinoma, lymphoma, melanoma,
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 CC bacterial parasitic, fungal, viral, protozoal and helminthic infections)
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
 CC of a test compound and in gene therapy. The present sequence is human
 CC PKIN-25 cDNA
 XX
 XX Sequence 995 BP; 255 A; 295 C; 253 G; 192 T; 0 U; 0 Other;
 SQ

Query Match 60.3%; Score 868; DB 6; Length 995;
 Best Local Similarity 100.0%; Pred. No. 7e-216;
 Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 CTTTGAATGGCCACCGGAATCTGAATCCAGAACCGTCTCATGTGCCAGAGGACATCTC 632
 DB 3 CTTTGAATGGCCACCGGAATCTGAATCCAGAACCGTCTCATGTGCCAGAGGACATCTC 62
 QY 633 AGAGCTGGAGACGGCTCAGAACTGCTGGAGTATCATAGGAACATCGTCAGGGTCATTCC 692
 DB 63 AGAGCTGGAGACGGCTCAGAACTGCTGGAGTATCATAGGAACATCGTCAGGGTCATTCC 122
 QY 693 CTCCTACCCCAAAATCCTCAAGTATCATAGTGTGACCGCCATGTGGAGCTTCTTA 752
 DB 123 CTCCTACCCCAAAATCCTCAAGTATCATAGTGTGACCGCCATGTGGAGCTTCTTA 192

QY 753 CCAGGCTCTGACCTATGTGTCCAAAGCAACCATCGTACTAATGCCCGCTTACCCTCAGGGT 812
 DB 183 CCAGGCTCTGACCTATGTGTCCAAAGCAACCATCGTACTAATGCCCGCTTACCCTCAGGGT 242
 QY 813 GCTGCTGCTGGGCTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGT 872
 DB 243 GCTGCTGCTGGGCTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGT 302
 QY 873 ATACAGGCTTGTCAATGTCTGTGTGGGCACTGTGAAGAGGCTGTGSCAGATAGGAC 932
 DB 303 ATACAGGCTTGTCAATGTCTGTGTGGGCACTGTGNAAGAGGCTGTGSCAGATAGGAC 362
 QY 933 CACGTTTGGGAGCTCATCGAGCCCTTCTTTGAAAGAGAGATGGCAGTTCCTGACAGCT 992
 DB 363 CACGTTTGGGAGCTCATCGAGCCCTTCTTTGAAAGAGAGATGGCAGTTCCTGACAGCT 422
 QY 993 CCTCATGAAGGTGTGAGCCAGGCTGTGACAGGAGTGTGATCCAGAAAGGCTGGGT 1052
 DB 423 CCTCATGAAGGTGTGAGCCAGGCTGTGACAGGAGTGTGATCCAGAAAGGCTGGGT 482
 QY 1053 GCTACACGGGCTCCCGGGGACCTCGACAGGCAACCTGCTGAACCGCTGGGCTTACAA 1112
 DB 483 GCTACACGGGCTCCCGGGGACCTCGACAGGCAACCTGCTGAACCGCTGGGCTTACAA 542
 QY 1113 TCCCAACAGGCTGTCTTCTGAAATGTCCTGAAATGTCCTGAAATGTCCTGAAATGTCCTGAAATGTCCT 1172
 DB 543 TCCCAACAGGCTGTCTTCTGAAATGTCCTGAAATGTCCTGAAATGTCCTGAAATGTCCTGAAATGTCCT 602
 QY 1173 GAGAAGATTCATCCAGTCACTGGGGAAGGTACCACTCATGTATGATGATGATGATGATGATGATGATGAT 1232
 DB 603 GAGAAGATTCATCCAGTCACTGGGGAAGGTACCACTCATGTATGATGATGATGATGATGATGATGATGAT 662
 QY 1233 CATGAGATCCAGGCTCGGCTCTCTGAGAACCCAAAGGATGCTGAGAGAGCAGTCAAGCT 1292
 DB 663 CATGAGATCCAGGCTCGGCTCTCTGAGAACCCAAAGGATGCTGAGAGAGCAGTCAAGCT 722
 QY 1293 GAAATGAGCTCTGCTTACAGGAATCTCAGCTGACTTGGAGCAGTGTGATGGGTGCGGCAT 1352
 DB 723 GAAATGAGCTCTGCTTACAGGAATCTCAGCTGACTTGGAGCAGTGTGATGGGTGCGGCAT 782
 QY 1353 CACCTCAATGGGAGGACGAGCCATACAGCTTTCGATATCATGAGAGTGGATCAT 1412
 DB 783 CACCTCAATGGGAGGACGAGCCATACAGCTTTCGATATCATGAGAGTGGATCAT 842
 QY 1413 TAATTCCTGCTCCCAAGAAATCCCTGA 1440
 DB 843 TAATTCCTGCTCCCAAGAAATCCCTGA 870

RESULT 12
 AA158051
 ID AA158051 standard; cDNA; 1778 BP.
 XX
 AC AA158051;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 254.
 XX
 KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200153312-A1.
 XX
 XX 26-JUL-2001.
 XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR P-PSDB; AAM40681.
XX

Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.

Claim 1; SEQ ID NO 3826; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the
encoded polypeptides (AAM38642-AAM42213) with neurotropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities, chemotactic/chemokinetic activity, haemostatic
activity/inhibin activity, cancer diagnosis and therapy, drug screening,
and thrombolytic activity, arthritis and inflammation, leukaemia and
C.N.S disorders. Note: The sequence data for this patent did not form
part of the printed specification

SQ Sequence 721 BP; 178 A; 212 C; 188 G; 143 T; 0 U; 0 Other;

Query Match 43.0%; Score 619; DB 4; Length 721;
Best Local Similarity 100.0%; Pred. No. 5.4e-151;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GCAATGGCTCTGCAAAACATCTGAACAGCAGTCTCTTCACTGGAGAACCTGATCTTA 279
DB 103 GCAATGGCTCTGCAAAACATCTGAACAGCAGTCTCTTCACTGGAGAACCTGATCTTA 162
QY 280 AATGAGTTTCTTATACGGCCACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTT 339
DB 163 AATGAGTTTCTTATACGGCCACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTT 222
QY 340 CCCAGCGCTGCTGCTCCAGCTGATTCAGGACCGCTGCTGAGAGGATTCATCAAG 399
DB 223 CCCAGCGCTGCTGCTCCAGCTGATTCAGGACCGCTGCTGAGAGGATTCATCAAG 282
QY 400 CAGGCTGGATTTGAGATGCGATTCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACC 459
DB 283 CAGGCTGGATTTGAGATGCGATTCCTGAGACGCTGAGCAGGCTCTGAGGATCCAGACC 342
QY 460 CTGGGGATCACACCCAGACACGTCATTGTGTGATGCTCCAGACAGGCTCTGATCGAG 519
DB 343 CTGGGGATCACACCCAGACACGTCATTGTGTGATGCTCCAGACAGGCTCTGATCGAG 402
QY 520 AGAACTTGGGAGAGATTCAGACCTCAAACTGGAGGATTTATCAGACACCTTCAC 579
DB 403 AGAACTTGGGAGAGATTCAGACCTCAAACTGGAGGATTTATCAGACACCTTCAC 462
QY 580 TGGCCACCGAATTCGAATTCAGAACCGTCTCATGTGCGAGAGACATCTCAGAGCTG 639
DB 463 TGGCCACCGAATTCGAATTCAGAACCGTCTCATGTGCGAGAGACATCTCAGAGCTG 522
QY 640 GAGACGCTCAGAAACTGCTGGAGTATCATAGGAACATCTGAGGATTCATTCCTCTTAC 699
DB 523 GAGACGCTCAGAAACTGCTGGAGTATCATAGGAACATCTGAGGATTCATTCCTCTTAC 582
QY 700 CCCAAATCTCAAAGTATCATAGTCTGACACGAGCATGTGTGACGCTCTTACAGGCT 759
DB 583 CCCAAATCTCAAAGTATCATAGTCTGACACGAGCATGTGTGACGCTCTTACAGGCT 642
QY 760 CTGACCTATCTCAAAGCAACCATCTGATTAATGCCCGCTTACCCGAGGCTGCTGCT 819
DB 643 CTGACCTATCTCAAAGCAACCATCTGATTAATGCCCGCTTACCCGAGGCTGCTGCT 702

QY 820 CTCGGGCTGTGGCAGTG 838
DB 703 CTCGGGCTGTGGCAGTG 721

RESULT 14
ABK71537
ID ABK71537 standard; cDNA; 615 BP.
XX
XX ABK71537;
XX
XX 30-JUL-2002 (first entry)
XX

Human dithp polynucleotide #3.
XX

Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
inflammatory disorder; viral infection; bacterial infection; seizure;
fungal infection; parasitic infections; developmental disorder; breast;
endocrine disorder; metabolic disorder; neurological disorder; cervix;
gastrointestinal disorder; transport disorder; gene therapy; kidney;
adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
skin; testis; thymus.

XX Homo sapiens.

XX WO200220754-A2.

XX 14-MAR-2002.

XX 29-AUG-2001; 2001WO-US027127.

XX 05-SEP-2000; 2000US-0229747P.
XX 05-SEP-2000; 2000US-0229748P.
XX 05-SEP-2000; 2000US-0229749P.
XX 05-SEP-2000; 2000US-0229750P.
XX 05-SEP-2000; 2000US-0229751P.
XX 05-SEP-2000; 2000US-0230583P.
XX 06-SEP-2000; 2000US-0230584P.
XX 06-SEP-2000; 2000US-0230514P.
XX 06-SEP-2000; 2000US-0230515P.
XX 06-SEP-2000; 2000US-0230517P.
XX 06-SEP-2000; 2000US-0230518P.
XX 06-SEP-2000; 2000US-0230519P.
XX 06-SEP-2000; 2000US-0230595P.
XX 06-SEP-2000; 2000US-0230597P.
XX 06-SEP-2000; 2000US-0230598P.
XX 06-SEP-2000; 2000US-0230599P.
XX 06-SEP-2000; 2000US-0230610P.
XX 06-SEP-2000; 2000US-0230865P.
XX 06-SEP-2000; 2000US-0230988P.
XX 07-SEP-2000; 2000US-0230951P.
XX 07-SEP-2000; 2000US-0231163P.
XX 07-SEP-2000; 2000US-0231167P.

(INCY-) INCYTE GENOMICS INC.

XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Moniyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI; 2002-383054/41.
DR P-PSDB; ABG59945.

An isolated polynucleotide useful in diagnostics and therapeutics.

Claim 1; Page 406; 686pp; English.

XX The invention relates to human diagnostic and therapeutic (dithp)
polynucleotides and their associated polypeptides (DITHP polypeptides).


```

Db      647 TACAAGCCACCTCCACCACATGGAGATCCAGCTCGCTCTCTGAGAACCCAAAGGATGCT 706
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QY      1336 TTGTATGGGTTCGGCCATCACCTCAATGGGACGAGGCCCATACACAGTCTTCGAATAC 1395
Db      767 TTGTATGGGTTCGGCCATCACCTCAATGGGACGAGGCCCATACACAGTCTTCGAATAC 826
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RESULT 2
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DEFINITION Sequence 1381 from Patent EP1293569.
ACCESSION AX714697
VERSION AX714697.1 GI:29889650
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.
TITLE Full-length cDNAs
JOURNAL Patent: EP 1293569-A 1381 19-MAR-2003;
Helix Research Institute (JP); Research Association for Biotechnology (JP)
FEATURES
source Location/Qualifiers
1. 1579
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 1440; DB 6; Length 1579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 30 ATGGAGCCCATATCGCCCGCACCTATCCCTCCCGGAGATGCCAGTACGGGAGGAG 89
Qy 61 AACCATATCTTCAGTTGATGACAGAACTGCTGGAGCACTCTGATCCACGACCGAA 120
Db 90 AACCATATCTTCAGTTGATGACAGAACTGCTGGAGCACTCTGATCCACGACCGAA 149
Qy 121 GATCCCATCCCTTCATGATCCAGCATTTGATGATGAGACAAACGACATGTGCCAGATT 180
Db 150 GATCCCATCCCTTCATGATCCAGCATTTGATGATGAGACAAACGACATGTGCCAGATT 209
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Db 270 CTGAACAGCAGTCTCTCCACCTGGAGAACCTGATCTTAATAGTGTTCCTATACGGCC 329
Qy 301 ACCGAAGCCAGAGGCTTTATCTGCAAGAGACAGTTCCTCCAGCGGCTGCTCGTCCAG 360
Db 330 ACCGAAGCCAGAGGCTTTATCTGCAAGAGAGACAGTTCCTCCAGCGGCTGCTCGTCCAG 389
Qy 361 CTGATTCAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCTGGATTTCTGGATGGC 420
Db 390 CTGATTCAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCTGGATTTCTGGATGGC 449
Qy 421 ATCCCTGAGCGGCTGAGCAGGCTCTGAGGATCCAGACCCTGGGATCACACCCAGACAC 480
Db 450 ATCCCTGAGCGGCTGAGCAGGCTCTGAGGATCCAGACCCTGGGATCACACCCAGACAC 509
Qy 481 GTCAATGCTGAGTGTCTCAGACACCGTCTGATCGAGAGAACTTTGGGGAAGAGATC 540
Db 510 GTCAATGCTGAGTGTCTCAGACACCGTCTGATCGAGAGAACTTTGGGGAAGAGATC 569

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QY	601	CAGAACCTCTCATGTCGCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG	660
Db	630	CAGAACCTCTCATGTCGCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG	689
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RESULT 3

AK057266	AK057266	1579 bp	mrna	linear	PRI 30-JAN-2004
LOCUS					
DEFINITION	Homo sapiens cDNA FLJ32704 f1s, clone TEST12000591, weakly similar to ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3).				
ACCESSION	AK057266				
VERSION	AK057266.1	GI:16552887			
KEYWORDS	oligo capping; f1s (full insert sequence).				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

REFERENCE
AUTHORS

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nagai, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Ishihara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Muraya, Y., Abe, K., Kamiyama, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Hirakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, K., Nakai, K., Yada, I., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs Nat. Genet. 36 (1), 40-45 (2004)

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JOURNAL
AUTHORSREFERENCE
AUTHORSJOURNAL
TITLEJOURNAL
COMMENT

3 Isogai, T., Otsuki, T. and Sugiyama, T. Direct Submission Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

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Homo sapiens chromosome 9 open reading frame 98, mRNA (cdna clone
MGC:35281 IMAGE:5175757), complete cds.

LOCUS

BC034776 GI:21961344

ACCESSION

BC034776

VERSION

1

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1656)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,

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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Faney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Green, E.D.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Schenker, Y.,

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Schneerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1656)
Straussberg, R.
Direct Submission
Submitted (24-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

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CDS

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ORIGIN

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RESULT 5

BC050576

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 2185)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2185)

Strausberg, R.

Direct Submission

Submitted (08-APR-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapsb@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: The I.M.A.G.E. Consortium

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-sbgc.stanford.edu>Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

FEATURES

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Best Local Similarity

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0; Indels

0; Gaps

0;

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VERSION
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.
Full-length cDNA sequences
Patent: EP 1308459-A 1657 07-MAY-2003;
Helix Research Institute (JP); Research Association for Biotechnology (JP)
FEATURES
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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VERSION AK093446.1 GI:21752320
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yaeuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Hara, H., Tanase, T., Nomura, Y., Toguchi, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mueshino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiya, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, P., Wakebe, H., Hishigaki, H., Watanabe, T.,

Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Wasuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
REFERENCE
AUTHORS
Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 1619)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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LOCUS AX211563 1452 bp DNA linear PAT 06-SBP-2001
DEFINITION Sequence 1 from Patent WO0159082.
ACCESSION AX211563
VERSION AX211563.1 GI:15523815
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kapeller-Libermann, R. and Chun, M.
TITLE 27802, an adenylate kinase
JOURNAL Patent: WO 0159082-A 1 16-AUG-2001;
Millemin Pharmaceuticals, Inc. (US)
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ORIGIN
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Best Local Similarity 86.5%; Pred. No. 2.7e-238;
Matches 1246; Conservative 0; Mismatches 2; Indels 192; Gaps 2;

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RESULT 9
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

FEATURES
source

BC079446 1581 bp mRNA linear ROD 15-SEP-2004
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BC079446
BC079446.1 GI:51260837
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Rattus norvegicus (Norway rat)

Rattus norvegicus
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Rattus.

1 (bases 1 to 1581)
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sánchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
Schurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

2 (bases 1 to 1581)
Director MGC Project.
Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov

Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 183 Row: a Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

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LOCUS	AX642974	
DEFINITION	AX642974	
ACCESSION	AX642974.1	GI:28550126
VERSION		
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
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AUTHORS	1	
	Yue, H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y., Gandhi, A.R., Tribouley, C.M., Walla, N., Yao, M.G., Lu, D.A., Greenwald, S.R., Ramkumar, J., Griffin, J.A., Kearney, L., Burford, N., Nguyen, D.B., Tang, Y.T., Baughn, M.R., He, A., Thornton, M., Hafalla, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F., Recipon, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M., Elliot, V.S., Thangavelu, K., Batra, S. and Ison, C.H.	
TITLE	Human kinases	
JOURNAL	Patent: WO 01096547-A 51 20-DEC-2001;	
FEATURES	Incyte Genomics, Inc. (US)	
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LOCUS AX211565 774 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 3 from Patent WO0159082.
ACCESSION AX211565
VERSION AX211565.1 GI:15523817
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Kapeller-Libermann, R. and Chun, M.
TITLE 27802, an adenylate kinase
JOURNAL Patent: WO 0159082-A 3 16-AUG-2001;
Millennium Pharmaceuticals, Inc. (US)
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Query Match 52.8%; Score 759.8; DB 6; Length 774;
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QY 757 GCTCTGACCTATGTCTCAAGACCACTCGTACTAATGCCCGTTCAACCCGAGGCTGCTG 816
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QY 817 CTCTCGGGCTGTGGGCAAGTCTCAGGCGCGCCCTCTCTGGCCCAAGAAATAC 876
Db 601 CTCTCGGGCTGTGGGCAAGTCTCAGGCGCGCCCTCTCTGGCCCAAGAAATAC 660
QY 877 AGGCTTGTCAATGTCTGTGGGCAACTGTCTGAAGAGGCTGTGGCAGATAGACCAAG 936
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Qy	937	TTTGGCAGCTCATCCAGCCCTCTTTTGAAGAGAGATGGCAG	979
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DEFINITION	Sequence 10688 from Patent WO02068579.		
ACCESSION	CQ724754		
VERSION	CQ724754.1	GI:42285611	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.		
REFERENCE	Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.		
AUTHORS	Kits, such as nucleic acid arrays, comprising a majority of		
TITLE	humanexons or transcripts, for detecting expression and other uses thereof		
JOURNAL	Patent: WO 02068579-A 10688 06-SEP-2002;		
FEATURES	PE Corporation (NY) (US)		
source	1. 577		
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Best Local Similarity	100.0%;	Pred. No. 2.9e-128;	Indels 0; Gaps 0;
Matches 577;	Conservative 0;	Mismatches 0;	
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Qy	463	GGGATCACACCCACAGACAGTCATTTGTCTGAGTGTCTCCAGACACGGCTCTTGATTCGAGAGA	522
Db	61	GGGATCACACCCACAGACAGTCATTTGTCTGAGTGTCTCCAGACACGGCTCTTGATTCGAGAGA	120
Qy	523	AACTTGGGGAGAGAAATCGACCTCAAACTGGAGAGATTATCAACACCTTTGACTGG	582
Db	121	AACTTGGGGAGAGAAATCGACCTCAAACTGGAGAGATTATCAACACCTTTGACTGG	180
Qy	583	CCACCCGAATCTGAATCCAGAACGGTCTCATCGTCCAGAGGACATCTCAGAGCTGGAG	642
Db	181	CCACCCGAATCTGAATCCAGAACGGTCTCATCGTCCAGAGGACATCTCAGAGCTGGAG	240
Qy	643	ACGGCTCAGAAAATCTGGAGTATCATAGGAAATCATCGTCCAGGGTCATTTCCCTCTACCC	702
Db	241	ACGGCTCAGAAAATCTGGAGTATCATAGGAAATCATCGTCCAGGGTCATTTCCCTCTACCC	300
Qy	703	AAAATCTCTCAAAGTCATCATGCTGTCGACGCCATGTGTGGACGTCCTTTACACAGGCTCTG	762
Db	301	AAAATCTCTCAAAGTCATCATGCTGTCGACGCCATGTGTGGACGTCCTTTACACAGGCTCTG	360
Qy	763	ACCTATGTCCAAAGCAACCATCGTACTAATGCCCCGTTCCACCCGAGGGTGTGTGCTGCTC	822
Db	361	ACCTATGTCCAAAGCAACCATCGTACTAATGCCCCGTTCCACCCGAGGGTGTGTGCTGCTC	420
Qy	823	GGGCTGTGGCAGTGGGAAAGTCTCGAGCGCGCCCTCTGGCGCGGAATACAGGCTT	882
Db	421	GGGCTGTGGCAGTGGGAAAGTCTCGAGCGCGCCCTCTGGCGCGGAATACAGGCTT	480
Qy	883	GTCAATGTCTGTGGGCAATCTGTGAAGAGGCTGTGGCAGATAGGACCAACGTTTGGC	942
Db	481	GTCAATGTCTGTGGGCAATCTGTGAAGAGGCTGTGGCAGATAGGACCAACGTTTGGC	540
Qy	943	GAGCTCATCCAGCCCTCTTTTGAAGAGAGATGGCAG	979
Db	541	GAGCTCATCCAGCCCTCTTTTGAAGAGAGATGGCAG	577

RESULT 14
BC062516
LOCUS
DEFINITION
Xenopus tropicalis hypothetical protein MGC76170, mRNA (cDNA clone MGC:76170 IMAGE:5335533), complete cds.
ACCESSION
BC062516
KEYWORDS
MGC.
SOURCE
Xenopus tropicalis (Silurana tropicalis)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 1674)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Shapletton, T.E., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Teohiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaney, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Mullany, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Rodriguez, S., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1674)
Klein, S. and Gerhard, D.S.
Direct Submission
Submitted (17-NOV-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angélique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 142 Row: e Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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ORIGIN
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Best Local Similarity 61.6%; Pred. No. 1.1e-122;
Matches 885; Conservative 0; Mismatches 552; Indels 0; Gaps 0;
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DB 66 CAGGAGAGTGTGTTGATATATTTCAGAAATGTTGGAAGAGTTCTTAGTGGACAGACCCAA 125
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DB 126 GACCAATCCAGTACATGATGATGATCTCTCCAAATGATATGATGATGATGATGAT 185
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721 AGTGTCTGACGAGGCAATGTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCAAC 780
726 AACGACAGGAGGCAATGTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCAAC 785
781 CATGTCTACTAATGCCCGTTACCCGAGGGTGTGTCTCGGGCTGTGGGAGTGGG 840
786 CCAAGTCTTGGCACTTCAACACCTCGAATATCTCTGTACGGGCCCCGGGAGTGGG 845
841 AAGAGTCTGAGGCGGCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGCTGTGGG 900
846 CGGAGGCTTCCAGGCGTGTGTCTGCGCGAGAAATGTGCAATGTCTCAACATTTGCTGTGGC 905
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1026 AGTAGTCTGGAGTCTGCTACACAGGCTGGGTGTGTACATGATTTCCAGAGACTGAC 1085
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1141 CCATTTGATTTCCATCATGAGGCGGCTGACTCTGAGAGAAATGTGATCCAGTCACTGGGAA 1200
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1266 AACCCAGGCAATTCGAGGAGGAGGCTCAGGCGAGGCTAGACATGTACACGCTAACGCC 1325
1321 GCTGACTTGGAGGAGTGTGTATGGGTGCGGCTATCACTCAATGGGAGGAGGAGGAGTAC 1380
1326 GAGGAGTGGAGGAGTGTGTATGGGTGCGGCTATCACTCAATGGGAGGAGGAGTAC 1385
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RESULT 15

CQ734872 1608 bp DNA linear PAT 03-FEB-2004
Sequence 20806 from Patent WO02068579.
CQ734872
CQ734872.1 GI:42324765
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Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 20806 06-SEP-2002;
JOURNAL

PE Corporation (NY) (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.4e-66;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: March 19, 2005, 22:35:43
Job time : 6115 secs

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